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Gaps between the contigs are represented as 100 N.
* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 120407)
                                                                                                                                                                   Similarity
                                                                                                ACATTITCIAAAACTCTITATAGIGAGAGCATAGGICTIAGGAAAAAATATATIAGCATT
ATGCACAATTGTGTATTAGATTCTGTGGCTAGCAAACGAAAAATTTTTCCAAGCTGACCTT
                                            AATAAGTAAATTGTCTCAAGTCATACTAAAGCACATTACTAGGATCAGTAAAAAATATAT
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                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
                                                                                                                                                                                                                        /clone="2242B18"
                                                                                                                                                                                                                                     map="4q22-q24"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                         .120407
                                                                                                                                                                                                                                                                                                                                 87654: contig of 87654 bp in length
87754: gap of 100 bp
107685: contig of 19931 bp in length
107785: gap of 100 bp
120407: contig of 12622 bp in length
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DQ027001
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AC021004
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AX7748405
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                                                                                                                                                                  Score 798.4; DB 12; Pred. No. 1.5e-235;
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                                                                                                                                                                                Length 120407;
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AR719430 Sequence
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AC021004 Homo sapi
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Homo sapiens BAC clone RP13-514E23
AC104059
AC104059.5 GI:18677542
    Direct Submission
Submitted (03-DEC-2001) Genome
University School of Medicine,
                                                                   2 (bases 1 to 165223)
Wang,C. and Cotton,M.
The sequence of Homo sapiens
Unpublished (2001)
                                                                                                                                      Hominidae, Homo.

1 (bases 1 to 165223)

Sulsron, J.E. and Waterston, R.

Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                            3 (bases 1 to 165223) Waterston, R.H.
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Eukaryota; Metazoa;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                  source
                                                                                                                                                                                                                                                                                                                 Pemale blood was obtained via a double-blind selection protocol. Female blood DNA was isolated from one randomly chosen donor (out of 10 female donors) and partially digested with a combination of ECORI and ECORI Methylase for library segments 1k2 or either MboI or DpnII for library segments 3k4. Size selected DNA was cloned into the pBACe3.6 vector between the ECORI sites for library segments 1k2 or the BamHI sites for library segments 3k4. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). The library has been arrayed into 384-well microtiter dishes and also gridded onto 22x22cm nylon high density filters for screening by probe hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MO 63108, USA 4 (bases 1 to Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE INFORMATION:

The RPCI-13 Human Female BAC Library was constructed using improved cloning techniques developed by Kazutoyo Osoegawa. The library was generated by Baohui Zhao in our laboratory. Construction was funded by a grant from the National Human Genome Research Institute (NHGRI, NIH) (#1RO1RG01165-03). The library was generated according to the new NHGRI/DOE 'Guidance on Human Subjects in Large-Scale DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Submitted (15-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 165223)
Waterston,R.
                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Feb 15, 2002 this sequence version replaced gi:18370036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restriction digest.
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                                                                                                                                                                                                       clone sequenced to the left is RP11-375K17.
s clone is at base position 1 of RP13-514E23;
e position 165223 of RP13-514E23.
                                                                                                                            from AC012208 was used to finish een AC012208 and AC104059.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
     organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                          location/Qualifiers
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                                                                                                                                                      AC104059. Polymorphisms exist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4749. .5171
/note="similar to Mus musculus
vw02e03.r1"
                                                                                                                                                                                                                                                                                               4890. .5494
/note="similar to
(NID:g17088280)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match to 4794. .5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4749. .5416
(Note="similar to Mus musculus EST BI697031
(NID:g15659660)"
                                                                                                                                                                                                                         vw97g06.r1"
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/note="similar to Homo sapiens EST H19314 (NID:g885554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4778. .4859
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                                                                           note="match to EST BG576372 (NID:g13584025)"
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1353. .4368
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2759. .3201
                                                                                                                                                                                                                                              note="similar to
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(NID:g15345757)"
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1916. .2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="L2"
1528. .1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375. .447
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="match to EST AA993990 (NID:g3180535) ou42a04:s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match to EST AW264096 (NID:g6640912) xq83f12.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'rpt_family="(TAGA)n"
| 774. 1819
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203. .3345
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                            BG204046 (NID:g13725733)'
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CAATGITATGITATTICITGCAACCCCTACACAAGGCCAAGAAATTACACAAGTACTAG
                                                                                                                                                                                                                                       GACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTTGATGAGGCACATTTACCCCTTTA
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                                                                                                                                                                                                                                                                                                                                                                 AAACACTAAGAATGAATGAGGGAAGAGGTAGCGGCTGAAAGGATTACTGAGCTCCACATT
                                                                                                                                                                                                                                                                                                                                                                                                                   AACCGGAGCCCATCTTGGTAGATGTTTCAACTATTGTCACATCAACCTTGAGAAGAGTTC 33079
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                                                         ATAAAACTAAAATCATTATAAGGACACAACCATGTGATATTTGTCCATCTGCTCTTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCACAATTGTGTATTAGATTCTGTGGCTAGCAAACGAAAAATTTTTCCAAGCTGACCTT
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7175.
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/note="similar to Mus musculus EST BB321301 (NID:g9029615)"
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/note="similar to
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Bardwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,

Baddwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,

Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,

Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,

Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Galagan,J., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,

McEwan,P., Waylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,

Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHOMO Sapiens chromosome 4 clone RP SEQUENCE, 12 unordered pieces. AC012208 AC012208.3 GI:8096853 HTG; HTGS PHASEL; HTGS DRAFT. Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661
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                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 26, 2000 this sequence version replaced gi:6454052. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Center project name: L1753
Center clone name: 375 K 17
Center clone name: 375 K 17
Center clone name: 375 K 17
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.96731
Consensus quality: 114873 bases at least Q40
Consensus quality: 1161974 bases at least Q30
Consensus quality: 170540 bases at least Q20
                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                    Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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me 4, clone
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7 map 4,
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WORKING DRAFT
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FEATURES
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Insert size: 174325; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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14863
14963
22018
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32502
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44214
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                                                     /estimated
32602. .447
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22018. .22117
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/db_xref="taxon:9606"
                   /note="assembly_fragment"
44214. .44313
                                                                                                   note="assembly_fragment"
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14963. .22017
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6520: contig of 2598 bp in length
6620: gap of 100 bp
14862: contig of 8242 bp in length
14962: gap of 100 bp
22017: contig of 7055 bp in length
22117: gap of 100 bp
22117: gap of 100 bp
32501: contig of 10384 bp in length
32501: contig of 10384 bp in length
32601: gap of 100 bp
44213: contig of 11612 bp in length
44213: gap of 100 bp
57141: contig of 12828 bp in length
57241: gap of 100 bp
1707: contig of 14466 bp in length
71807: gap of 100 bp
1707: contig of 15911 bp in length
7181: gap of 100 bp
175425: contig of 3260 bp in length
120578: gap of 100 bp
175425: contig of 54847 bp in length
00cation/Qualifiers
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                                                                                                                                           CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACACAAGTACTAG
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vector_side:right"
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Pred. No. 4.6e
0; Mismatches
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4.6e-235;
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420

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137354

540

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137234

136994 720 660

137114

137054

600

300

240

137474

180

137534

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JOURNAL COMMENT
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AUTHORS
TITLE
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G49140/c
                                    ORIGIN
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 Query Match
Best Local Similarity
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primer_bind
primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                    Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TTTGTGTAGGGGTTGCAAGAAAT
Primer B: CCACATTGACTTGATGGTCAAAA
STS size: 282
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781
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1 (bases 1 to 401)
Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., C
Unpublished (2000)
                                                                                                                                                             BAC
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SHGC-79840 Human Homo
G49140
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STS.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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KCl:
Tris-HCl:
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                                                                                                                          organism="Homo sapiens"
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sapiens
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ACCESSION
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AC154950
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AC154950.2 GI:68265244
HTG: HTGS_PHASE1; HTGS_DRAFT;
Bos taurus (cattle)
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Bos taurus clone CH240-42G8,
unordered pieces.
                                                                                                                                                                                                                                                                                                                       Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 206504)
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
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Pasternak, S., Paul, H., Perez, L., Pfankoch, C., Plopper, F., Poindexter, A., Pepovic, D., Primus, E., Pu, L. L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L., Plazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Retlly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Reilly, M., Ren, Y., Reuter, M., Rose, M., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shett, J., Shetty, J., Shevery, S., Scott, G., Shatsman, S., Shen, H., Sheed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sheed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sheed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walter, B., Wang, J., Wang, O., Wargh, S., Warren, R., Wei, X., White, F., Wang, Q., Wang, S., Warren, R., Wei, X., White, F., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, D., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Rivant, C., Shang, J., Shang, S., Smith, D.R., Holt, R.A., Smith, H.O., Rivant, S., Smith, D.R., Holt, R.A., Smith, H.O., R., Marker, B., Smith, D.R., Holt, R.A., Smith, H.O., R., Marker, B., Smith, R., Woon, L., Smith, R., Woon, L., Smith, R., Walter, B., Smith, R., Walter, B., Smith, R., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig separated individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            table.
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On Jun 28, 2005 this sequence version replaced gi:57164422.
The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-JAN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(bases 1 to 206504)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                            (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 29 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                Center project name: FCEU
Center clone name: CH240-42G8
Center clone name: CH240-42G8
Center clone name: CH2640-42G8
Assembly program: Atlas 3.0;
Consensus quality: 195434 bases at least Q40
Consensus quality: 197609 bases at least Q30
Consensus quality: 197609 bases at least Q20
Consensus quality: 199501 bases at least Q20
Estimated insert size: 200872; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                              Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
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                                              /estimated_length=unknown 6557. .6838
                                                                                            /estimated_length=50
5784. .5883
                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-42G8"
                                                                                                                                                                                                                                                                                         organism="Bos taurus"
estimated_length=282
.0957. .11006
                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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of 10444 bp in length
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TITLE JOURNAL REFERENCE AUTHORS TITLE

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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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LOCUS
DEFINITION
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AC137121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11419 ATGTATATGTACTAATGTGTGCTATATTTTGTAGACTGCAAATGTAAAGATTTTTCTGTG 11478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469
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        AC137121 181548 bp DNA linear ROD 16-OCT-2
Mus musculus chromosome 5, clone RP23-286M22, complete sequence.
AC137121
                                                                                                                                                                                                                                                                                                                                              TTCATTACTTAATGCCAAATAATTACGTTTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCĂTTCĂAAAGGGCĂAGGĂGACTGAĂĂTCATTAGAGGGAAACAGGTA-ATCTAACTGGTT 11824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCTCCACATTGACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTTGATGAGGCAC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTTTTACTACACCATTTTTAGTCTTTTCTTTCTGAATTACTTCATTACTTCCTTGTAGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATATGCTTGATAAGCA-----GTATTATTGACTGCAATCTCTCCTTAAGGCCAAGAAAA 11879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAGTTCAAACACTAAGAATGAATGAGGGAAGAGGT----AGCGGCTGAAAGGATTACT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAAATTTATCCTTCATCCACAGGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATCANAA---GAAATAAAACTAAAATCATTATAAGGACACAACCATGTGATATTTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCACCCTTTA-----ATCAGATTATGCTAATATTTCTTCAAGATT---CTTTGTTA 11705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTACCCTTTAGCCCATGTTAACATTTTCTTCAGGATTCATTACTATTAAAATTATTTA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACTCCACACTGAGGTGGTGGTCAAGAGGGCATTATGGATCTGAATTTTGATGAGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGACTTTAATTGGACCCCGTTGTGGTTAAGGCTTCAACTACTGTCACATCAACCTTAGG
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19769. .49818
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14769. .14818
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Pred. No. 8.8e-61;
0; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185;
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                                                                                          ROD 16-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (CB 3 (bases 1 to 181548)

Research, 320 Charles Street, Cambridge, MA 02141, USA (CB Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galaggan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Galaggan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Galaggan, J., Gardyna, S., Graham, L., Karatas, A., Kells, C., Lievine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Machett, R., Nicola, R., Norbu, C., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren,B., Nusbaum,C. and Lander,E.
Chromosome 5, clone RP23-286M22
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Submitted (17-AUG-2004) Whitehead Institute/MIT Center
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
Contact: Project Information
Center project name: L26408
Center clone name: 286_M_22
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complement(6813. .6853)
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RESULT 7.
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Allen, C., Allen, H., Albrocoks, S., Andin, M., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balawin, D., Bandaranaike, D., Batberr, M., Barnstead, M., Benahmed, F., Balswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Ernet, C., Chi, J., Chacko, J., Chacko, J., Chen, G., Chen, G., Chen, G., Chen, Z., Chi, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souzà, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delyado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evens, C.A., Garrer, M., Foster, P., Francer, C.M., Escotto, M., Eugene, C., Evens, C.A., Garrer, M., Foster, P., Francer, C.M., Escotto, M., Bugene, C., Evens, C.A., Garrer, M., Foster, P., Francer, C.M., Gabisi, M., Gall, R., Grady, M., Guerra, W., Guerra, W., Gubrata, W., Hanlot, C., Hamilton, C., Hamilton, K., Hanlot, K., Harwey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Have, Y., Havlak, P., Hawes, A., Hunderson, M., Hernandez, J., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Hunderson, M., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Hunderson, M., Hernandez, J., Hu, Y., S., Kally, S., Kelly, S., Martin, K., Martin, R., Martin, R., Martin, R., Martin, R., Milosan', Jevic, A., Martin, K., Martin, K., Martin, R., Milosan', Jevic, A., Morris, K., Morris, K., Morris, K., Morris, K., Paste, K., Senth, M., Scherer, S., Statsmar, S.
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AC141145.3 GI:29568005
HTG; HTGS_PHASE1; HTGS_DRAFT.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 206606)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baylor Plaza, Houston, TX 77030, USA
On Apr 5, 2003 this sequence version replaced gi:28913313.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chémistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 19161 bases at least Q40
Consensus quality: 195784 bases at least Q30
Consensus quality: 195987 bases at least Q30
Estimated insert size: 195646; sum-of-contigs estimation Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hgsc-help@bcm.tmc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
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67348 contig of 2798 bp in length
70246 contig of 2798 bp in length
70346 gap of unknown length
70346 gap of unknown length
70368 contig of 2792 bp in length
73168 gap of unknown length
7639 gap of unknown length
81355 contig of 3371 bp in length
81353 gap of unknown length
90585 contig of 5329 bp in length
90585 gap of unknown length
90585 contig of 5352 bp in length
90585 gap of unknown length
90585 contig of 5352 bp in length
90585 gap of unknown length
104621 contig of 5194 bp in length
104621 gap of unknown length
11746 gap of unknown length
120264 contig of 625 bp in length
120364 gap of unknown length
120364 gap of unknown length
120364 gap of unknown length
134349 contig of 6108 bp in length
13429 contig of 6474 bp in length
134349 gap of unknown length
140554 gap of unknown length
140554 gap of unknown length
140554 gap of unknown length
156077 contig of 6028 bp in length
16626 contig of 10249 bp in length
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51799: contig
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54374: contig
54474: gap of
58651: contig
58751: gap of
61150: gap of
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PRANCINE DESANLIS, ALAIN FOURNIER, ISABELLE MAURY, QING ZHOU LIU PC

C12N15/09,A61K39/395,A61K45/00,A61P7/10,A61P9/00,A61P25/00, PC
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AX027295.1 GI:10188271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                           GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAATTC
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ilarity 97.7%;
Conservative
                                                                                                                   Conservative
                                                                                                                                                                                                       /codon_statt=1
/proteIn_id="CAC09126.1"
/proteIn_id="CAC09126.1"
/db_xrefE="d1:10188272"
/db_xrefE="d1:10188272"
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SDCTLKIILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEM
VRHKILFPGRDYIDQMNKVIGOLGTPCDEFMKKLQPTVRNYVENFFXXGLTFPKLFP
DSLFPADSGHNKLJASQARDLLSKMLVIDPAKKRISVDDALQHPYINVWYDPAEVEAPP
PGLYDKQLDEREHTIEFMKELIYKEVMNSEEKTRNGVVKGQPSPSGAAVNSBESLPPS
SSVNDISSMSTDQTLASDTDSSLEASAGPLGCCR"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                         note="unnamed protein product"
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Pred. No. 4e-14;
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Pred. No. 4e-14;
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WO0043524.
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PN JP 20
PD 23-OC
PF 05-OC
PF 05-OC
PF 03-OC
PR 05-OC
PR 
                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                       CQ892479 .
Sequence 56 from Patent
CQ892479
CQ892479.1 GI:55165021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unclassified sequences.
1 (bases 1 to 1505)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J.,
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified
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Weihe, E.D., Schaefer, M.K.,
                                                       Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD078044.1 GI:22623647
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C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-1998 JP 2000514991
03-OCT-1997 US 60/060995
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Key Location/Qualifiers
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JP 2001519146-A/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unidentified"
/mol_type="genomic DNA"
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Pred. No. 3.9e-14;
0; Mismatches 2
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     Gillen, C.,
     Wetzels, I.
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     and Wnendt, S
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Matches 84; Conserv
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AR380407
Yang, D.D.

JNK3 modulators and methods of use Patent: US 6943000-A 1 13-SEP-2005;
                                                                                                            Sequence 1 from
AR716219
AR716219.1 GI:7
                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1505)
Cocks, B.G., Stuart, S.G. and Seilhamer, J.
Compositions for the detection of blood
response gene expression
patent: US 6607879-A 952 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
Location/Qualifiers
                              1 (bases 1 to 1505)
Davis,R.J., Flavell,R.A., Rakic,P.,
                                                           Unclassified
                                                                        Unknown
                                                                                                                                                 AR716219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown
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Patent: EP 1469316-A
Gruenenthal GmbH (DE)
                                                                                     Unknown.
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/mol_type="genomic DNA"
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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                                                                                                                                  1505 bp
patent US 6943000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        patent
                                                                                                                                                                                                                                                                                                           Score 82.8; DB 2;
Pred. No. 3.9e-14;
0; Mismatches 2;
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US 6607879
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                                  Whitmarsh, A.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunological
                                    Kuan, C.-Y.
                                                                                                                                                 PAT 07-OCT-2005
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HSU34819/c
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AX377861/c
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                         AUTHORS
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Sequence
AX377861
          1 (bases 1 to 1505)
Gupta,S., Barrett,T.,
Derijard,B. and Davis,
                                                                                          Homo sapiens
                                                                                                                                                      HSU34819
Human JNK3 alpha2 protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.
 Selective interaction
                                                                                                                                U34819.1
                                                                                                                                            U34819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening method Patent: WO 0212338-A 56 14-FEB-2002; Gruenenthal GmbH (DE)
                                                 Hominidae; Homo.
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gillen, C., Wetzels, I., Wnendt, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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1. .1505
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                                                                                                                                GI:1463124
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic
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Pred. No. 3.9e-14;
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RESULT 17
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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Collins, F. S., Wagner, L., Shemmen, C. M., Schuler, G. D.
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Uddin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              1850 bp mRNA linear Homo sapiens mitogen-activated protein kinase 10, mAGE:5721954).
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Submitted (25-AUG-1995) Roger J. Davis, Molecular Medicine,
University of Massachusetts Medical School; 373 Plantation Street,
Worcester, MA 01605, USA
                                                                                                                                                                                                                         Hominidae; Homo.

1 (bases 1 to 1850)
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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EMBO J. 15 (11), 2760-2770 (1996)
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                                                                                                                                                                                                                                                                                                                                                       sapiens (human)
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DNQFYSVEVGDSTFTVLKRYONLKFIGSGAQGIVCAKAYARLAKHYNMSKSKV
DNQFYSVEVGDSTFTVLKRYONLKFIGSGAQGIVCAKAYARLAKHYNMSKLTQMQ
THAKRAYRELUMKCVNHKNIISLLNVETPGKTLEEFQDVYLVMELMOALCQVIQME
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSF
MMTPYVVTRYYKAAPEVILGMGYKENVDIMSVGCIMGEMVRHKILFFGRDYIDONNKVI
EQLGTPCPEFMKKLQPTVRNYVENRPKYAGDTFPKLFPDSLFPADSEHNKLKASQARD
LISKMLVIDPAKRISVDDALQHFYINVMYDPAEVGAPDPGIYDKQLDRERETIEEWKE
ELIYKEVUNSEEKTKNGVVKGQPSPSGAAVNSSESLPPSSSVNDISSNSTDQTLASDTD
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/protein_id="AAC50604.1"
/db_xref="GI:1463125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="UNK protein kinase isoform that phosphorylates the transcription factor c-Jun on Ser-63 and Ser-73; protein
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68. .1462
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1. .1505
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Pred. No. 3.9e
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3.9e-14;
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mRNA (cDNA clone
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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                               84;
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20986507.

Location/Qualifiers
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Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter.N., Bouffard,G.G., Beren,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (26-JAN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaithersburg, Maryland,
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                                                                                                                                                ATTACTTCCTTGTAGATAAGTTCTTT 854
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue type="Ovary, pooled from 3 adults"/clone Tib="NIH MGC_125"
/lab_host="DH10B"
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97.7%;
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Pred. No. 3.
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                                            Submitted (04-707).

Submitted (04-707).

Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:flj-cdna@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDD human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotute, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamira, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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/organism="Homo sapiens'
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JNK3-controller and method of using the same Patent: JP 2001519146-A 2 23-OCT-2001; UNIVERSITY OF MASSACHUSETTS
                                                                          1 (bases 1 to 2366)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J.,
                                                                                                                                       unidentified
                                                                                                                                                                         BD078045.1 GI:22623648 JP 2001519146-A/2.
                                                                                                                                                                                                                               BD078045 2366 bp I
JNK3-controller and method of using
                                                                                                                  unclassified sequences.
                                                                                                                                                         unidentified
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                                                            Yang, D.D.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/db_xref="taxon:9606"
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/note="cloning vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="BRSSN2008125"
/tissue_type="substantia nigra"
/clone_lib="BRSSN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.8e-14;
0; Mismatches 2
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Pred. No. 3.8e-14;
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                                                                            Kuan, C.Y. and
                                                                                                                                                                                                                                                     PAT 27-AUG-2002
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Best Local Similarity

Matches 84; Conserv
                                                                                                                         Query Match
Best Local Similarity
Matches 84; Conserv
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Sequence 3 !
AR716220
AR716220.1
                                                                                                                                                                                                                                                     JNK3 modulators and methods of use Patent: US 6943000-A 3 13-SEP-2005; University of Massachusetts and Yale University; Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis, R.J., Flavell, R.A., Rakic, P., Whitmarsh, A.J.,
                                                                                                                                                                                                                                                                                                                                            Unclassified
                                                                                                                                                                                                                                                                                                                                                           Unknown.
                                                                                                                                                                                                                                                                                                                                                                         Unknown.
                                                                                    GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                    ATTACTTCCTTGTAGATAAGTTCTGT 711
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DERK DI YANG
                                                                                                                           Conservative
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Location/Qualifiers
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03-OCT-1997 US 60/060995
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JP 2001519146-A/2
23-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism='Unidentified'
                                                                                                                                                                                            /organism="unknown"
/mol_type="genomic |
                                                                                                                                                                                                                                          Location/Qualifiers
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from patent US 6943000.
                                                                                                                                     10.3%;
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                                                                                                                      Score 82.8; DE
Pred. No. 3.8e-
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Pred. No. 3.
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.8e-14;
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BC051731/c
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                                                                                                               source
                                                                                                                                     through the I.M.A.G.E. Consortium/LLNL at: http://image.llr
Series: IRAK Plate: 90 Row: k Column: 24
This clone was selected for full length sequencing because
passed the following selection criteria: matched mRNA gi: 2
                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH MGC Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. S
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          /tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
                                                    /organism="Homo sapiens"

/mol_type="mKNA"

/db_xref="raxon:9606"

/clone="MGC:50974 IMAGE:4838495"
                                                                                                                         ocation/Qualifiers
note="Vector: pBluescriptR"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheefetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Bucterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                              cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiral Toshiyuki and Piero Carninci (RIKAN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 943 Web Site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcc@paxil.stanford.edu Contact: (Dickson, Mark) mcc@paxil.stanford.edu Contact: (Dickson, Mark) mcc@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2494 pp mRNA linear Homo sapiens mitogen-activated protein kinase 10, MGC:50974 IMAGE:4838495), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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found
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mRNA gi: 20986509

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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 84;
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AR454561
AR454561.1
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Loring,J.F., Tingley,D.W. and Edwards,C.M.
Genes expressed in alzheimer's disease
Patent: US 6602888-A 34 27-JAN-2004;
Incyte Corporation; Palo Alto, CA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified
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                                                       ATTACTTCCTTGTAGATAAGTTCTTT 1710
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|/68. .1727
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/db_xref="HGNC:6872"
/db_xref="IMGT/GENE-DB:6877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 from patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRD 
LKESNIVKSDCTLKILDFLARTAGTSFMMTFYUVTRYYRAFBYILGMGYKENVDMW 
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SVGCIMGEMIKGAVLFGCLARTAGTSFMMTVIGTFCFERMKKLQFTVRNYVENRFKYA 
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GLTFFKLFFDSLFFADSSHNKLKASQARDLLSKMLVIDFAKRISVDDALGHFY 
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DPASVBAPFPQIYDKQLDERSTTIEFMKELIYKENDALGHFY 
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DPASVBAPFPQ
                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSSESLPPSSSVNDISSMSTDQTLASDTDSSLEASAGPLGCCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MAPK10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:42688030
                                                                                                                                                                                                                                                                                                      10.3%;
97.7%;
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_xref="IMGT/GENE-DB:6872"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _xref="MIM:602897"
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Pred. No. 3.7e-14;
0; Mismatches 2;
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Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2677 bp
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                                                                                                                                                                                                                                                                                                                                   Length 2677;
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COMMENT
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REFERENCE
ORIGIN
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LOCUS
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RESULT 24

the following selection criteria: Location/Qualifiers

mRNA gi: 20986504

/organism="Homo sapiens"
/mol\_type="mRNA"
/mol\_type="mRNA"
/db\_xref="taxon:9606"
/clone="IMAGE:4792270"
/tissue\_type="Brain, hypothalamus"
/clone\_lib="NHH\_MGC\_96"

note="Vector: pBluescript"

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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,
Villalon, D.K., Muzny, D.M., Sodergren, F.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, F.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, F.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Mitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
12477917
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 8
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site: (Dickson, Mark) mcd@paxil.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Contact: (Dickson, Mark) Topickson, Mark) Rodriquez, A., and Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Director MGC Project.
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1 (bases 1 to 2678)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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protein kinase 10, mRNA (cDNA clone
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CA 94305
                                                                                                                                                                                                                                                                   Myers,
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JOURNAL
PUBMED
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AUTHORS
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

RIausmer, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heich, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

NAL Proc., Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                          Direct Submission
Submitted (31-UL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirak
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: d Column: 6
This clone was selected for full length sequencing because it
                                                                                                                                                                  http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECU3505/
HOMO sapiens mitogen-activated protein kinase MGC:41877 IMAGE:5261221), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTACTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 2690)
                                                                                                                                        Stephanie Rodrigues,
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Pred. No. 3.7e-14;
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                                                                                                                                        Amy Sanchez
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                                                                                                                                        Mark Ketteman, Anuradha and Michelle Whiting
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mRNA (cDNA clone
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ACCESSION
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CS206710/c
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Query Match
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                                                                                                                                                                            Spittaels, K.F.
Patent: WO 2005109001-A 11 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 from Patent CS206710
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             passed the following selection criteria: matched mRNA gi: 20986509. Location/Qualifiers
                                                                                                                                                                                                                                                            Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                      CS206710.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="MAPK10 protein"
/protein_id="AAH35057.1"
/protein_id="AAH35057.1"
/db_xref="GeneID:5602"
/db_xref="GeneID:5602"
/db_xref="MIM:662897"
/db_xref="MIM:662897"
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/translation="MSLINFLYYCSEPTLDVKIAFCQGFDKQVDVSYIAKHYNMSKSKV
DNQFYSVEVGDSTFTVLKRYQNLKFIGSGAQGIVCAAYDAVLAWLAKHKLSRPFQNQ
DNQFYSVEVGDSTFTVLKRYQNLKFIGSGAQGIVCAAYDAVLCMVALKKLSRPFQNQ
DNQFYSVEVGDSTFTVLKRYQNLKFIGSGAQGIVCAAYDAVLCMVALKKLSRPFQNQ
DNQFYSVENGVLKKKCVMHKNIISLLNVFTPQKTLEEFFQDYVLWMELMDAVLCQVIQME
LDHEENSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILPFDRDYIDQMKKVI
MMTPYVVTRYYRAPEVILGNGYKENVDIWSVGCINGEMVRHKILFFDRDYIDQMKKVI
                                                                         /organism="Homo sapiens"
/mol_type="unassigned DNi
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLEASAGPLGCCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARD
LLSKMLVI DPAKRISVDDALQHPY I NVWYDPAEVEAPPPQI YDKQLDEREHTI EEWKE
                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="MIM:602897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonyms: p493F12, p54bSAPK, JNK3A, FLJ12099, JNK3"
/db_xref="GeneID:5602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="MAPK10"
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/clone="MGC:41877 IMAGE:5261221"
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Pred. No. 3.7e-14;
0; Mismatches 2
    Score 82.8; DB 2; Pred. No. 3.7e-14;
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WO2005109001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagahari, K., Mutakami, K., Kabuda, I., Lwayanagi, I., Mayanagi, I., Mayanagi, I., Mayanagi, I., Mayanagi, I., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Manda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Kikkawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Harakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fuji, A., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fuji, A., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiolata, N., Sato, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoyuchi, H., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, T., Sugiyama, A., Takeura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inaggaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Nakajima, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakajima, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakajima, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakajima, Y., Shirai, Y., Takahashi, Y., Nakagawa, Y., Sanashita, R., Nakai, Y., Nakai
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                                                                                                                                                       Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Kikuchi, H., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project
Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,
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3081 bp mRNA linear PRI 20-JAN-2006 Homo sapiens cDNA FLJ42801 fis, clone BRCAN2001223, highly similar co MITOGEN-ACTIVATED PROTEIN KINASE 10 (EC 2.7.1.-).
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                                                                                                                                                                                  Submitted (04 JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized step-codon. The CDS has been directionally cloned using BD In-Pusion(TM) cloning system between the Sall and HindIII sites of the DNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.
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Hines, L., Rolls, A., Jepson, D., Moreira, D., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Williamson, J. and LaBaer, J.
Direct Submission
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Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and LaBaer, J.
Cloning of human full-length CDS in Creator (TM) recombinational
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1269 bp mRNA linear SYN 22-MAR-2
Synthetic construct Homo sapiens clone FLH117970.01X
mitogen-activated protein kinase 10 (MAPKIO) mRNA, complete cds.
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ff]-cdna@nifty.com, Tel:81-438-22-3975, Fax:81-438-52-3986) NNEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction; Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; Clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; 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                                                                                                                                                   Location/Qualifiers
organism="synthetic construct"
/mol_type="mRNA"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRCAN2001223"
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/clone_Tib="BRCAN2"
/note="cloning vector: pME18SFI
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Pred. No. 3
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Zuo,D., Taycher,E.
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JOURNAL REFERENCE
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SOURCE
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VERSION
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Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
cxpression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). The CDS has been directionally cloned using
BD In-Fusion(TM) cloning system between the Sall and HindIII sites
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
after Sall site and before 'ATC' to provide Kozak consensus
sequence; 'GG' after last codon and before HindIII site to maintain
reading frame. Each clone is clonally isolated and full-length
sequence-verified.
                                                                                                                                                                                                                                                     Direct Submission
Submitted (05-JAN-2005) Biological Chemistry and Molecular Submitted (05-JAN-2005) Biological Chemistry and Molecular Standard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
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Synthetic construct Homo sapiens clone FLH020610.01L
mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.
AY890997
                                                                                                                                                                                                                                                                                                                                                                           Hines,L., Rolfs,A., Jepson,D., Moreira,D., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Williamson,J. and LaBaer,J.
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synthetic construct
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Human ORF Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector system
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DNGFYSYBVGDSTFTVLKRYOMLKFIGSGAQGIVCAKDATAKHYNMSKSKY
THAKRAYRELVLMKCVHKHKNIISLLVUFTPOKTLBEFODVYLVMELMDALKLSRPEQNO
LDHERMSYLLYOMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSF
EMTPYVVTRYYRAPEVILGMGYKENVDIMSVGCIMGEMVRHKILFFGRDYIDOMNKVI
EQLGTPCPEFMKKLQPTVRNYDXAGLTFFKLFPDSLFPADSEHNKLKASQARD
LLSKMLVIDPAKRISVDDALOHFYINVMYDPAEVEAFPPQIYDKOLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKGQPSPSAQVOQ"
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/transT_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AAX41509.1"
/db_xref="GI:61158132"
/db_xref="GI:61158132"
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note="derived from Homo sapiens first strand cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (05-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). The CDS has been directionally cloned using
BD In-Fusion(TM) cloning system between the Sall and HindIII sites
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
                                                                                                                                                                                                                                                                                                                                                                      Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F. Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and LaBaer,J.
Cloning of human full-length CDS in Creator (TM) recombinational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                   2 (bases 1 to 1269)
Hines, L., Rolfs, A., Jepson, D., Moreira, D.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y.,
Williamson, J. and LaBaer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic construct Homo sapiens clone FLH117966.01L mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other sequences; artificial sequences.
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DNQFYSDVLDRNVAIKLSRPFQNQ
THAKRAYRELVLMKCVNHKNIISLLAVFTSQKTLDEFQDVALDRNVAIKKLSRPFQNQ
THAKRAYRELVLMKCVNHKNIISLLAVFTSQKTLEEFQDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIIVWKSDCTLLIDFGLAFTAGTSF
MMTPYVVTRYKKLQDTVRAVYUMFRYYAGLIFFRLFPSLFPADSEHNKLKASQARD
EQLGTPCPEFRKKLQDTVRAVYUMFRYAGLIFFRLFPSLFPADSEHKLKASQARD
LLSKMLVIIDPAKRISVDDALQHFYINWYDPAEVEAPPQIYDKQLDEREHTIEEMKE
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/protein_id="AAX42931.1"
/db_xref="GI:61366953"
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/transl_table=11
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//ab_host="Bscherichia coli DH5alpha Tl resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
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Pred. No. 2.2e-13.
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clone FLH117966.01L
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and
                                                                                                                                                                     2 (bases 1 to 1269)
Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J.,
Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
Direct Submission
                                                                                                                                                                                                                                                                                     1 (bases 1 to 1269)
Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
Cloning of human full-length CDS FLEXGene in
Gateway (TM) recombinational vector system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitogen-activated protein kinase 10 (MAPK10) mRNA, AY893302
AY893302.1 GI:60815280
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Synthetic construct Homo sapiens clone FLH057665.01X
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DTAKKAYRELVLMKCVNHKNIISLLANUFTPQKTLEEFGDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLLRTAGTSF
MMTPYVVTRYYRAFBVLIGMGYKENVDIMSVGCIMGEMVRHKILFPGRDYIDQWNKVI
EQLGTPGDEFMKKLQPTVRNYVENRFKYAGLTFPKLFFDSLFPADSEHNKLKASQARD
LLSKMLVIDPAKRISVDDALQHFYINVMYDPAEVEAPPPGIYDKQLDEREHTIEEMKE
LIYKEVMNSEEKTKNGVVKGQPSPSAQVQQL"
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/transl_table=11
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/lab_host="Escherichia coli DH5alpha Tl resistant"
/note="derived from Homo sapiens first strand cDNA
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Pred. No. 2.2e-13;
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LOCUS
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Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fus
                                                                                                                                               Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J. Direct Submission
                                                                                                                                                                                                                                                                                        1 (bases 1 to 1269)
Hines, L., Taron, B., Jepson, D., Moreira, D., Re
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and I
Cloning of human full-length CDS FLEXGene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY893752 1269 bp mRNA linear (Synthetic construct Homo sapiens clone FLH057664.01L mitogen-activated protein kinase 10 (MAPKIO) mRNA, pa
                                                                                                   Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
                                                                                                                                                                                                                                         Gateway(TM)recombinational vector system Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY893752.1 GI:600
Human ORF Project
                                                                                                                                                                                                                                                                                                                                                                                      other sequences; artificial sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                     (bases 1 to 1269)
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/tcansl_table=11
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="nat/36339.1"
/protein_id="nat/36339.1"
/db_xref="qI:60815281"
/translation="MSLHFLYYCSEPTLDVKIAFCQGFDKQVDVSYIAKHYNMSKSKV
DNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQNQ
THAKRAYRELVLMKCYNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLGGIKHLHSAGIHHRDLKPSNIVVKGCTLKILDFGLARTAGTSF
MMTPYVVTRYKLAGAYRENDIMSVGLTFPKLFPGBSEHNKLKASQARD
EQLGTPGDEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPKALGDTLGWAKASQARD
LLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVMNSBEKTKNGVVKGQPSPSAQVQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
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/mol_type="mRNA"
/db_xref="taxon:32630"
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Pred. No. 2.2e-13;
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d LaBaer,J.
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BT019710/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     630
                                                                         2 (bases 1 to 1269)

Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kalnine, N., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Direct Submission
                                                                                                                                                                                                                                                 1 (bases 1 to 1269)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenst Kalnine,N., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B7019710
Synthetic construct Homo sapiens mitogen-activated protein kinase 10 mRNA, partial cds.
Submitted (28-OCT-2004) BD Biosciences Clontech, 1020 East Meadow circle, Palo Alto, California 94303, USA
This CDS clone is a part of a collection of human full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BT019710
BT019710.1 GI:54696287
FLI_CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct synthetic construct
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                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                 vector
                                                                                                                                                                                                                                                                                                                                                                                  other sequences; artificial sequences
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/transl_table=1:1
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/product="mitogen-activated protein kinase 10"
/protein_id="max36789.1"
/protein_id="max36789.1"
/db_xref="dI:60827197"
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/translation="MSLHFLYYCSEPTLDVKIAFCQGFDKQVDVSYIAKHYMMSKSKV
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/thakayrelylmkcvikkniisllnverpQkTleEPQDVYLVMSLMDANLCQVIQME
THAKRAYRELYLMKCVIKHKNIISLLNVETPQKTLEEPQDVYLVMSLMDANLCQVIQME
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSOTTMKILFGGRDYIDQMNKVI
EDLGTPCPEFMKKLQPTVRNVYENRPKYAGLTFPKLFPDSLFPAJSEHHKLKASQARD
EQLGTPCPEFMKKLQPTVRNVYENRPKYAGLTFPKLFPDSLFPAJSEHHKLKASQARD
LLSKMLVIDPAKRISVDDALQHPYINVMYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKGQPSPSAQVQQD"
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note="derived from Homo sapiens first strand cDNA library
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one="FLH057664.01L"
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Pred. No. 2.2e-13;
0; Mismatches 1;
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Best Local
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                                                                                                                                                                                             Hominidae; Homo.

1 (bases 1 to 1306)

Desanlis, F., Fournier, A., Maury, I. and Liu, Q.Z.

Polypeptides derived from JNK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the DNR-DDAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
PR 20-JAN-1999 FR 99/00586,26-FEB-1999 US 60/122175 PI FRANCINE DESANLIS,ALAIN FOURNIER,ISABELLE MAURY,QING ZHOU LIU PI C12N15/09,A61K39/395,A61K45/00,A61P7/10,A61P9/00,A61P25/00, PC
                                             PR PR
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        BD249786.1 GI:33059556
JP 2002534982-A/22
                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides derived from JNK3.
BD249786
                                                                                                                                                      Patent: JP 200253;
AVENTIS PHARMA SA
                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                    Homo sapiens (human)
JP 2002534982-A/22
22-OCT-2002
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                                             19-JAN-2000 JP 2000594932
20-JAN-1999 FR 99/0058
                                                                                                                                                                          JP 2002534982-A 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSLHFLYYCSEPTLDVKIAFCQGFDKQVDVSYIAKHYNMSKSKV
DNQFYSEVGDSTFTYUKRYQNLKPIGSGAQGIVCAAYDAVLLRNVAIKKLSRPFQNQ
THAKKAYRELVLMKCYNHKNIISLLAVFTPQKTLEEFQDVYLVMELMDALKLSRPFQNQ
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSF
MMTPYVVTRYYKADFVILGMGYKENVDIWSVGCIMGEWVRHKILFBRDSEHRKLKASQARD
EQLGTPCPEEFMKKLQDTYRNYVENRFXYAGLTPFKLFPSLFPADSEHKLKASQARD
LDLSKMLVIDPAKRISVDDALQHPYINVMYDPAEVEAPPPQIYDKQLDEREHTIEEMKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="mitogen-activated protein kinase
/protein_id="AAV38516.1"
/db_xref="GI:54696288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="BD Creator(TM) CDS Library derived from MGC
collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:32630"
/clone="GH01307L1.0"
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/note="Vector: pDNR-Dual"
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Pred. No. 2.
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AUTHORS
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JOURNAL
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AX027293/c
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AR430629/c
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Sequence 22 from Patent
AX027293
AX027293.1 GI:10188269
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                         Homo sapiens (human)
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Fournier, A., Maury, I., Zhou-Liu, Q. al
Polypeptides derived from JNK3
Patent: US 6649388-A 22 18-NOV-2003;
Aventis Pharma S.A.; Antony;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A61P25/14,
PC A61P25/16, A61P25/28, C07K16/40, C12N1/15, C12N1/19, C12N1/21
, C12N5/10, C12N9/12,
PC C12Q1/02, C12Q1/48, C12N15/00, C12N5/00
CC Polypeptides derived from JNK3
PH Key Location/Qualifiers
FT CDS (142) (1291
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
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                                                                                                                                                                                   CTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                     CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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ilarity 98.8%;
Conservative
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Location/Qualifiers
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1. .1306
                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
/mol_type="genomic DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 2.2e-13;
0; Mismatches 1;
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Pred. No. 2.2e-13;
D; Mismatches 1
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                                                                                         1306 bp
WO0043524.
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US 6649388.
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BD078046/c
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JNKS-controller and method of using the same Patent: JP 2001519146-A 3 23-OCT-2001;

UNIVERSITY OF MASSACHUSETTS

OS Unidentified
PN JP 2001519146-A/3
PD 23-OCT-2001
PF 05-OCT-1998 JP 2000514991
PF 03-OCT-1997 US 60/060995
PR 03-OCT-1998 UP 60/060995
PR 03-OCT-1997 US 60/060995
PR 03-OCT-1998 UP 60/060995
PR 03-OCT-1997 US 60/060995
PR 03-OCT-1998 UP 60/060995
PR 03-OCT-1988 UP 60/060995
PR 03-OCT-1988 UP 60/060995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unclassified sequences.
1 (bases 1 to 1773)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
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BD078046.1
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JNK3-controller and method of using the same.
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Patent: WO 0043524-A 22 27-JUL-2000;
AVENTIS PHARMA SA (FR) ; DESANLIS FRANCINE (FR) (FR) ; FOURNIER ALAIN (FR) ; MAURY ISABELLE (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
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DAVLCRWALKSRPFQNQTHAKRAYRELVLMKCYNHKNIISLLNVFFPQKTLEEFQ
DVYLVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHHSAGIIHRDLKPSNIVVK
SDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMGYKENVDLWSVGCIMGEM
VRHKILFPGRDYIDQMNKVIEQLGTFCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFP
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PQIYDKQLDEREHTIEEWKELIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ"
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/db_xref="taxon:9606"
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db_xref="GI:10188270"
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                                                                                                                                                                                                                                                                                                                                                                                        A FLAVELL, PASKO RAKIC, ALAN
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?.2e-13;
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AR716221/c
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CQ892477/c
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VERSION
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AR716221
AR716221.1 GI:77364282
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Yang, D.D.

JNK3 modulators and methods of use Patent: US 6943000-A 4 13-SEP-2005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening method
Patent: EP 1469316-A 54 20-OCT-2004;
Gruenenthal GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54 from Patent CQ892477 CQ892477.1 GI:55165020
                                     Unclassified.
1 (bases 1 to 1773)
Davis,R.J., Flavell,R.A., Rakic,P.,
                                                                                                                                                        AR716221
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                                                                              Unknown
                                                                                          Unknown.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Similarity 98.8%;
81; Conservative
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Location/Qualifiers
1...1773
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNJ
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 2.1e-13;
0; Mismatches 1;
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Pred. No. 2.1e-13;
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EP1469316.
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                                        Whitmarsh,
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                                        ,Α.J.,
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                                        Kuan, C.-Y.
                                                                                                                                                         PAT 07-OCT-2005
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ORGANISM
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HSU34820/c
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AX377859/c
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Hominidae; Homo.

1 (bases 1 to 1773)

Gupta,S., Barrett,T., Whitmarsh,A.J.,
Derijard,B. and Davis,R.J.
Selective interaction of JNK protein
                                                                                      Homo sapiens (human)
                                                                                                                                                HSU34820 1773 bp
Human JNK3 alphal protein kinase
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Sequence 54 from Patent
AX377859
                                                                                                                           U34820.1
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
                                                                                                                                        U34820
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gruenenthal GmbH (DE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
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                                                                                                                           GI:1463126
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic D
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Pred. No. 2.1e-13;
0; Mismatches 1.
                       Whitmarsh, A.J., Cavanagh, J., Sluss, H
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Pred. No. 2.1e-13;
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WO0212338.
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(JNK3A1) mRNA, complete
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                                                               Catarrhini;
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                                                                         Euteleostomi;
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                                                                                                                                                                PRI 25-JUL-1996
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CQ714411/c
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AUTHORS
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Best Local S
Matches 81
                                                                                                                                  AUTHORS
TITLE
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Sequence 345 from Patent
CQ714411
CQ714411.1 GI:42275268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-AUG-1995) Roger J. Davis, Molecular Medicine, University of Massachusetts Medical School, 373 Plantation Street, Worcester, MA 01605, USA
Derijard, B. Cell 76, 1025-1037, 1994
Sluss, H. K. Mol. Cell. Biol. 14, 8376-8384, 1994.
Location/Qualifiers
                                                                Patent: WO 02068579-A 345 06-SEP-2002; PE Corporation (NY) (US)
                                                                                              thereor
                                                                                                              Kits, such as nucleic acid humanexons or transcripts,
                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
                                                                                                                               Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a
                                                                                                                                                                            Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription factors
EMBO J. 15 (11), 2760-2770
8654373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                          CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTGAATTCATTA 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="msilflycseptldyklafcqgfdkqvdvsylakyhmskskv
DNQFYSYBVGDSTFTVLKRYQNLKFIGSGAQGIVCAAYDAVLDRUVAIKKLSRFFQNQ
THAKRAYRELVLMKCYNHKNIISLLAVFTPGKTLEEFQDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLCGIIHLHSBAGIIHBDLKPSNIVVKSDCTLKILDFGLARTAGTSF
LDHERMSYLLYQMLCGIIHLHSBAGIIHBDLKPSNIVVKSDCTLKILDFGLARTAGTSF
MATPYVVTRYYRAPEVILGMGYKENVDIMSVGCIMGEMVRHKILFFGRDYIDOMNKVI
EQUETPCPEFMKKLQPTVRNYVENRPKYAGLTFFKLFPDSLFPADSEHNKLKAASQARD
LLSKMLVIIDPAKRISVDDALGHFYINWYDDFAEVEAPPPQIYDKQLDEREHTIEEMKE
LIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ"
/organism="Homo sapiens"
/mol_type="unassigned DNA"
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="UNK protein kinase isoform that phosphorylates the transcription factor c-Jun on Ser-63 and Ser-73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="JNK3 alpha1 protein kinase"
/protein_id="AAC50605.1"
/db_xref="GI:1463127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 2.1e-13;
0; Mismatches 1;
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                                                                                                                                                                                                              Euteleostomi;
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other uses
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RESULT 44
CS206711/c
LOCUS
                                                                                                               REFERENCE
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ORGANISM
                                                                                                                                                                                            DEFINITION
ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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ACCESSION
VERSION
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AR709626/c
                                                        FEATURES
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                                                                                    AUTHORS
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                    Spittaels, K.F.
Patent: WO 2005109001-A 12 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR709626
Sequence
AR709626
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                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                          Sequence 12
CS206711
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              CS206711.1 GI:83412266
                                                                                                                                                                                                                                                     CS206711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 2131)
Levine,Z. and Bernstein,J.
Variants of protein kinases
Patent: US 6936450-A 87 30-AUG-2005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compugen Ltd.; Tel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR709626.1
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                             Location/Qualifiers
1. .2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                        from Patent
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Pred. No. 2.1e-13;
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Pred. No. 2.1e-13;
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WO2005109001
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Best Local :
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                                                                                                                                                                                                                                                                                                                                          PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                          Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irié, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishil, S., Yamamoto, J., Salto, K., Kawai, Y., Isono, Y., Nakamura, Y., Ishil, S., Yamamoto, J., Salto, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Kikkawa, K., Pujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi, Fujii, A., Hara, H., Tanase, T.O., Nomura, Y., Togiya, S., Komai, F., Hara, R., Fakeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Prita, M., Toshikawa, Y., Musanhino, K., Yuuki, H., Oshima, A., Sasaki, N., Sano, S., Moniyama, H., Satoh, N., Takahai, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Tanigami, A., Pujiwara, T., Ono, T., Yamada, K., Fujii, Y., Komiyama, M., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzuni, Y., Fujimori, Y., Kohatake, N., Inagaki, H., Ikama, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, A., Hikiji, T., Kobatake, N., Itakana, H., Watanabe, A., Hikiji, T., Kobatake, N., Nagawa, T., Matanabe, T., Nakajima, Y., Takahashi, Y., Kawabata, A., Hikiji, T., Kobatake, N., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Ya
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  Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T., Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R., Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S., Terashima,Y., Watanabe,M., Sujiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Sato,H., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Kawai,Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK057723.1 GI:16553642 oligo capping; fis (full insert sequence)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Similarity 98.8%;
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                                                                                                                                                                                                                                                                                                                                                                    Genet. 36 (1), 40-45 (2004)
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Pred. No. 2.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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KEYWORDS
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Best Local S
Matches 81
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JNK3-controller and method of using the same
JNK3-controller and method of using the same
Patent: JP 2001519146-A 4 23-OCT-2001;
UNIVERSITY OF MASSACHUSETTS
OS Unidentified
PN JP 2001519146-A/4
PD 23-OCT-1998 JP 2000514991
PF 05-OCT-1998 JP 2000514991
PR 03-OCT-1997 US 60/060995
PR ROGER J DAVIS, RICHARD A FLAVELL, PASKO RAKIO
PI COLINIS/09, A01K67/027, A61K31/711, A61K45/00, J
PC A61P21/00,
PC A61P21/00,
PC A61P25/08, A61P25/14, A61P25/16, A61P25/28, C1:
C12Q1/68,
PC G01N33/15, G01N33/50, C12N15/00, C12N5/00
PC Strandedness: Double;
CC JNK3-controller and method of using the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1260
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JNK3-controller and method of using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unclassified sequences.
1 (bases 1 to 2372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified
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NEDO human cDNA sequencing
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           Topology: Linear;
JNK3-controller and method of using the same
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C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
                                                                                                                                                                                                                                                                                 05-OCT-1998 JP 2000514991
03-OCT-1997 US 60/060995
ROGER J DAVIS,RICHARD A FLAVELL, PASKO RAKIC,ALAN J WHITMARSH
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                                                                                                                                               A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C12Q1/48, PC
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/tissue_type="uterus"
/clone_lib="UTERU2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="cloning vector: pME18SFL3"
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Pred. No. 2.1e-13;
0; Mismatches 1;
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PAT

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Isogai, T., Otsuki, T. and Sugiyama, T.

Direct Submission

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(B-mail:flj-cdna@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center. National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evaluation; clone selection for full insert sequencing: RAB and
CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
                                                                                                                                                                                                                             Length 2156;
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BD078048/c
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                                                                                             Query Match
Best Local Similarity
Matches 81; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  Patent:
UNIVERSI
OS Uni
OS Uni
PP 05-
PF 05-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unclassified sequences.

1 (bases 1 to 2372)

Davis_R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J.,
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BD078048.1 GI:226
JP 2001519146-A/5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JNK3-controller and method of using the same Patent: JP 2001519146-A 5 23-OCT-2001;
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JNK3-controller and method of
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                           CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAATTCATTA 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ent: JP 2001519146-A 5 2:
ERSITY OF MASSACHUSETTS
                                                                                                   10.1%;
llarity 98.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROGER J DAVIS, RICHARD A FLAVELL, PASKO RAKIC, ALAN J WHITMARSH CHIA YIN KUAN, CHIA YIN KUAN, DERK DI YANG CI2N15/09, A01K67/027, A61K31/711, A61K45/00, A61K48/00, A61P9/10, A61P21/00, A61P25/14, A61P25/16, A61P25/28, C12N5/10, C12Q1/48, PC.
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Location/Qualifiers
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03-OCT-1997 US 60/060995
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23-OCT-2001
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                                                                                                                                                                                                                                                                                                                            /organism='Unidentified'
Location/Qualifiers
                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Unclassified.
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(bases 1 to 2372)
(bases 1 to 2372)
Land Seilhamer, J. J.
Au-Young, J. and Seilhamer, J. J.
Composition for the detection of signaling pathway
Patent: US 6500938-A 1389 31-DEC-2002;
Patent: Ganomics, Inc.; Palo Alto, CA;
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Sequence
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Patent: WO 2005109001-A 9 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels,
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/mol_type="genomic DNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Search completed: July 19, 2006, 20:10:46 Job time: 5076 secs
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Unknown.
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Unclassified.
1 (bases 1 to 2372)
1 (bases 1 to 272)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.-Y. and Yang,D.D.
JNK3 modulators and methods of use Patent: US 6943000-A 6 13-SEP-2005;
University of Massachusetts and Yale University; Boston, MA
Location/Qualifiers
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                                                                                                                                                                                                                                                    24-JUL-2003; 2003US-0490234P
25-NOV-2003; 2003US-00723681
25-NOV-2003; 2003US-0525239P
  Identifying risk of, preventing and/or treating breast identifying and/or analyzing polymorphic variations in
                                                                              WPI; 2005-163257/17
                                                                                                                          Roth RB, Nelson MR,
Hoyal-Wrightson CR;
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25-NOV-2003;
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                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENOM INC
                                                                                                                                                                                                                                                                                                                  TTAAAATTATTTATGAAAAAGTTTTTGTCCTGGATCATTACCATCAGAATAATCAGAATG
                                                                                                                                                                                                                                                                                                                                                                                       TTTGATGAGGCACATTTACCCTTTAGCCCATGTTAACATTTTCTTCAGGATTCATTACTA
CACAGGGAAATTCATTACTTAATGCCAAATAATTACGTTTTGATG
                                                                                                                   GAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTACTTCCT
                                                                                                                                                                      TTTGATGAGGCACATTTACCCTTTAGCCCATGTTAACATTTTCTTCAGGATTCATTACTA
                                                    TGTAGATAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATC
                                                                TGTAGATAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATC
                                                                                                     GAGAAGGCTGTCCTTTACTACACCATTTTTAGTCTTTTCTTGAATTCATTACTTCCT
                                                                                                                                                        AATGCCACACTGAATATCAAAAGAAATAAAACTAAAAATCATTATAAGGACACAACCATGT
                                                                                                                                                                                                                                                                AATGCCACACTGAATATCAAAAGAAATAAAACTAAAATCATTATAAGGACACAACCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003US-0490234P.
2003US-00723681.
2003US-0525239P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2004WO-US016939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n MR,
CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/standard_name= "Single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                     57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    617pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; 112 G;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 463.4;
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                                                                                                       .5e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 U; 1 Other
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Indels Length

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Gaps

60

395 0

465 800

> 420 755 360 695 300 635 240 575 180 515 120 455

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                                                                                                                                                                                                         Query Match
Best Local S
Matches 84
JNK3; c-jun N-terminal kinase 3; JNK3alphal isoform; JNK3alpha2 isoform;
                                       07-NOV-2000
                                                                                                                                                                                                                                               Sequence 1281 BP; 390 A; 297 C; 305 G; 289 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            The invention relates to a process for preparing recombinant stre activated protein kinase b (SAPK b) using Escherichia coli. This encodes a recombinant stress-activated protein kinase b associate
                  DNA encoding c-jun N-terminal kinase 3 derivative JNK3deltaNalpha2
                                                          AAA59380
                                                                             AAA59380 standard;
                                                                                                                                                                                                                                                                                                                                      Process for preparing recombinant stress-activated protein kinase b (SAPK b) using Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KR99081424-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant protein; stress-activated protein kinase b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding recombinant stress-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK50805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK50805 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                   (GLDS )
                                                                                                                                                                    1142
                                                                                                                                                                                                                                                                                                                                                                            2000-661807/64.
                                                                                                                                                989
                                                                                                                                                                                                         84;
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                    AAU79884.
                                                                                                                                                                                                                                                                                                                                                                                                                    LG CHEM LTD
                                                                                                                                                                              GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC
                                                                                                                                       ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                   GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                            ATTACTTCCTTGTAGATAAGTTCTTT 1057
                                                                                                                                                                                                                                                                                                                                                                                                 Choo
                                                                                                                                                                                                                                                                                                                   Fig 1;
                                                                                                                                                                                                         Conservative
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                       98KR-00015362
                                                                                                                                                                                                                                                                                                                                                                                                                                                          98KR-00015362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "SAPK b"
/note= "Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   9pp; Korean.
                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                 10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                 Yoon
                                                                             1422
                                                                                                                                                                                                                                                                                                                                                                                                HS,
                                                                                                                                                                                                         0;
                                                                                                                                                                                                        Score 82.8; D
Pred. No. 5.8e
0; Mismatches
                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                               Chung
                                                                                                                                                                                                                                                                                                                                                                                                王;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stress-activated
                                                                                                                                                                                                                            BG
                                                                                                                                                                                                                   8e-09;
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                                                                                                                                                                                                                          Length 1281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase
                                                                                                                                                                                                                                                                             ori. This sequence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPK b; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAPK b).
                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                stress-
                                                                                                                                                                                                         Gaps
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RESULT 7 AAX37266/c ID AAX37266

standard;

DNA; 1505

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XXXXXX

20-MAR-2003 21-JUL-1999 AAX37266;

(revised)
(first entry)

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Query Match
Best Local Similarity
                                                                                                                               Matches
                                                                                                                                                                                                                       The specification describes derivatives of JNK (c-jun N-terminal kinase) 3, which have deletions from the N-terminal region corresponding to positions 1-38 of the JNK3alphal and alpha2 isoforms or a c-terminal deletion from position 139. JNK are mitogen-activated kinases implicated in neurodegeneration and apoptosis of neurons. The derivatives are used to identify specific ligands. These ligands, and JNK3-specific antibodies, are used for prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's, Parkinson's or Huntington's diseases, degeneration associated with aging or acquired immune deficiency syndrome, brain injury, or cerebral anoxia, hypoxia or edema. Vector containing sequences encoding the derivatives are useful in gene therapy, e.g. of spinal cord injury and retinal degeneration. The present sequence encodes the derivative JNK3deltaNalpha2
                                                                                                                                                                                            Sequence 1422 BP; 436 A; 322 C; 329 G; 335 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitogen-activated kinase; neurodegeneration; apoptosis; neuron; neurodegenerative disease; Alzheimer's; Parkinson's; brain injury; Huntington's disease; aging; acquired immune deficiency syndrome; cerebral anoxia; hypoxia; edema; gene therapy; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 46-48; 57pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New derivatives of c-jun ligands for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desanlis F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-1999;
26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JAN-2000; 2000WO-FR000104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200043524-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS PHARMA SA
1223
                                                                1283
                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degeneration; ss.
                                                             GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTGAATTC
                                                                                               GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                              ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                             Conservative
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99US-0122175P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "JNK3deltaNalpha2"
                                                                                                                                            10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-terminal kinase 3, useful for identifying neurodegeneration, have specific deletions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maury
                                                                                                                             ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          French.
                                                                                                                                            Score 82.8; DB 3; Pred. No. 5.9e-09;
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ή,
1198
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                                                                                                                                                          Length 1422;
                                                                                                                               Indels
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                                                                           RESULT 8
ABL88412/c
BXXX
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                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for identifying compounds that modulate CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method CC comprises (a) incubating a cell that can express a JNK3 protein, or that CC thas JNK3 activity, with a compound under conditions and for a time CC compound; (b) incubating a control cell under the same conditions and for cclivity without the compound; (c) measuring JNK3 expression/CC activity in the cell in the presence of the compound; (d) comparing the CC amount of JNK3 expression/activity in the presence of the compound; (d) comparing the CC indicates that the compound modulates JNK3 expression/activity. The CC invention also provides a transgenic non-human mammal having a transgene CC disrupting expression of a JNK3 gene, the transgene being chromosomally CC integrated into germ cells of the mammal. JNK3 expression inhibitors; CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, Parkinson's CC amyotrophic lateral sclerosis, trauma, motorneuron disease, Parkinson's CC disease or epilepsy. The present sequence represents the nucleic acid Sequence of human JNK3 (GenBank accession numbers UJ4820, U07620, L27128, L35236, X12740 and CC U0727 can also be used in the method of the invention. (Updated on 20-the present sequence under the compounce of the mammal conditions.)
                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches ·84
                                                                                                                                                                                                                                                                                                                                      Sequence 1505 BP;
16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY09200
                              ABL88412;
                                                             ABL88412 standard; cDNA; 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of c-Jun N-terminal kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; disorder; Alzheimer's disease; Huntington disease; amyotrophic lateral sclerosis; ischemia; trauma; motorneuron disease; Parkinson's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYMA-) UNIV MASSACHUSETTS
                                                                                                                                            1263
                                                                                                                                                                            989
                                                                                                                                                                                                                                                                        .84
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                                                                                                                                          GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                      ទ
                                                                                                                                            ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                                                                                                                           ATTACTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                              GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                      correct
                                                                                                                                                                                                                                                                     10.3%;
llarity .97.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of JNK3 (GenBank Accn No: U34819).
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0060995P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US020904
                                                                                                                                                                                                                                                                                                                                     459 A; 343 C;
                                                                                                                                                                                                                                                                                                                                                                      DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rakic P,
                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                     Score 82.8; D
Pred. No. 6e-0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      346
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                                                                                                                                                                                                                                                                                                                                      357
                                                                                                                                                                                                                                                                                      6e-09;
                                                                                                                                                                                                                                                                                                     DB 2; Length 1505;
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                                                                                                                                                                                                                                                                       <u>ب</u>
                                                                                                                                                                                                                                                                                                                                     U; 0 Other;
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                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                            1264
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RESULT 9
ADI31626/c
ID ADI316
XX
AC ADI316
XX
TO 17-JUN
TO Human
XX
KW Human;
KW Crohn'
KW Crohn'
KW acute
WW osteop

(first

ADI31626

standard;

CDNA; 1505

ΒP

0

Human cDNA #952 17-JUN-2004

Human; gene; ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteograthritis; rheumacoid arthritis; acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;

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                                                                                                                 Matches
                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                 The invention relates to identifying pain-regulating substances (A) comprises (i) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analyssic activity. (A) along with nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB8506-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, pain; pain; pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention
                                                                                                                                                                            Sequence 1505
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gillen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2000DE-01037759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2001; 2001WO-EP009011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200212338-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHEF ) GRUENENTHAL GMBH
                                                        1323
1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-257469/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulated cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analgesic; gene therapy; neurological disorder;
                                                                                                                84;
                                                                            GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                ATTACTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                               Fig 34; 213pp; German.
ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                        GCACCTGAAGGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wetzels I,
                                                                                                                 Conservative
                                                                                                                                                                          B₽;
                                                                                                                                                                            459 A; 343 C;
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                                                                                                                              10.3%;
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                                                                                                                 Score 82.8; D
Pred. No. 6e-0
0; Mismatches
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                                                                                                                                                                            346 G;
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                             711
                                                                                                                                                                             357
                                                                                                                               8; DB 6
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                                                                                                                   2;
                                                                                                                                                                             U; 0 Other;
                                                                                                                                              Length 1505;
                                                                                                                   Indels
                                                                                                                   0
                                                                                                                   Gaps
                                                           1264
                                                                                       685
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RESULT 10
ADS83693/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC hybridisation complexes and comparing the levels of the detected comprision complexes with the level of hybridisation complexes with the level of hybridisation complexes correlates with the presence of an comparing the levels of the detected comprision complexes correlates with the presence of an complexes correlates with the presence of an comprision complexes correlates with the presence of an comprision of the detected probes. The collaboration and a plurality of detectable complexes and a comprision of the comprision of target polynurality of polynucleotide probes. The collaboration of the diagnosis of an immunopathology, such as Crohn's disease, asthma, concertive colitis, hypereosinophilia, irritable bowel syndrome, concerative colitis, hypereosinophilia, irritable bowel syndrome, concerative colitis, rheumatoid arthritis or acute monocytic leukaemia, and in concerning agents for the treatment of the diseases. The microarray may concerning agents for the treatment of the diseases. The microarray may concerning agents for the treatment of the diseases. The composition concerning also be used in drug discovery and development, toxicological and concerning also be used in purification of a subpopulation of mrnas, cDNAs or genomic fragments. This sequence represents a human CDNA, of the composition of the printed specification but was obtained in electronic format directly from the printed specification but was obtained in electronic format directly from the printed specification but was obtained in electronic format directly from the printed specification but was obtained in electronic format directly from the printed specification but was obtained in electronic format directly from the printed specification but was obtained in electronic format directly from the printed specification of a subspecification of a
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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                                                                   ADS83693 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or osteoarthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-895307/82
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                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                               GTACCTGAAGGAAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                              ATTACTTCCTTGTAGATAAGTTCTGT 711
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                                                                   CDNA;
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                                                                   ВP
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RESULT 11
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Matches
                                                              Human MAPK10,
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ADS83693

amyloid-beta precursor protein; pharmaceutical; mitogen activated protein-kinase inhibitor; neu

neurological disease;

transcript variant 2

DNA.

(first entry)

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Query Match
AEG09274 standard; DNA; 2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a human lymph node cDNA used to detect blood cell and immunological response gene expression. Note: The present sequence does not appear in the printed specification but was obtained in electronic format from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunopathological conditions, such as AIDS, allergies, anaemia, asthma, atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polynucleotides which are used as probes to detect genes differentially expressed in an immunological response, abundantly expressed in an immunological response and/or coding for a polypeptide known to regulate blood cell biology. The polynucleotides are useful in research and diagnostic applications particularly in cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaems; asthma; atherosclerosis; bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (seqdata.uspto.gov/sequence.html?DocID=20040077003).
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                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                               GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                       ATTACTTCCTTGTAGATAAGTTCTGT 711
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Pred. No. 6e-0
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mitogen activated protein-kinase inhibitor in admixture with a carrier.

The method involves activation of a biological pathway producing an indicator of the processing of amyloid-beta precursor protein e.g. a indicator of the processing of amyloid-beta precursor protein e.g. a indicator induces the expression of a reporter e.g. alkaline phosphatase, of the pharmaceutical composition further comprises a label indicating use of the composition for treating or preventing a condition involving cognitive impairment or a susceptibility to the condition. The agent is useful in the manufacture of a medicament for inhibiting the processing of amyloid-beta precursor protein in a subject suffering from or susceptible to the abnormal processing of the protein, or for treating or preventing a condition, preferably, Alzheimer's disease. This sequence encodes human mitogen-activated protein kinase 10 (MAPKIO), transcript variant 2, a kinase involved in the up-regulation of amyloid-beta 1-42.
                                                                                           Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method of identifying a compound that inhibits the processing of amyloid-beta precursor protein in a mammalian cell. The invention also describes; a) an agent for inhibiting amyloid-beta precursor processing consisting of an antisense polynucleotide; a ribozyme or a small interfering RNA (siRNA), where the agent comprises a nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence encoding the polypeptide comprising the amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical, composition comprising the agent for inhibiting amyloid-beta precursor processing or an amyloid-beta precursor processing or an amyloid-beta precursor processing-inhibiting amount of a processing of the polypeptide comprising the agent for inhibiting amyloid-beta precursor processing-inhibiting amount of a processing of the polypeptide composition comprising the agent for inhibiting amyloid-beta precursor processing-inhibiting amount of a processin
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                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2006-231019/24.
P-PSDB; AEG09283.
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24-AUG-2004; 2004US-0603948P.
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                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                             2211
GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                Conservative
                                                                                                                                                                                                                                                                                             ₽P;
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transcript variant 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                             674 A; 498
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Pred. No. 6
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GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC

Conservative

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GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC

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RESULT 12
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ID AXX37
XX AXX37
XX AXX37
XX DT 20-MA
DT 20-MA
DT 21-JU
XX C-Jun
KW C-Jun
KW Lische
KW human
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                                                                                                                                                                                                     The invention relates to a method for identifying compounds that modulate CC c-Jun N-terminal kinase 3 (JNKJ) expression or activity. The method CC comprises (a) incubating a cell that can express a JNKJ protein, or that CC sufficient for the cell to express a JNKJ protein and for a time CC sufficient for the cell to express a JNKJ protein/activity without the CC compound; (b) incubating a control cell under the same conditions and for activity in the cell in the presence of the compound; (c) measuring JNKJ expression/ CC activity in the cell in the presence of the compound; (d) comparing the CC indicates that the compound modulates JNKJ expression/activity in the presence and absence of the CC indicates that the compound modulates JNKJ expression/activity. The CC integrated into germ cells of the mammal having a transgene CC disrupting expression of a JNKJ gene, the transgene being chromosomally integrated into germ cells of the mammal JNKJ expression inhibitors, CC e.g. antisense nucleic acids, are used to treat disorders involving capturing the gene cells, captured to treat disorders involving CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, ischemia, CC disease or epilepsy. JNKJ sequences under GenBank accession numbers CC disease or epilepsy. JNKJ sequences under GenBank accession numbers (c) field** (d) 4820, U07620, L27128, L35236, X12740 and V00727 can be used in CC field** (d) 4820, U07620, L27128, L35236, X12740 and V00727 can be used in contract DR
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Query Match
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                                                                                                                     Sequence
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                                                                                                                                                                                  the method field.)
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21-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification of c-Jun N-terminal kinase 3 modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1999
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Local Similarity
nes 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                           2367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flavell RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first en
                                                                                                                           BP;
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                                                                                                                           712 A; 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                         10.3%;
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Score 82.8; DB 2;
Pred. No. 6.6e-09;
0; Mismatches 2;
                                                                                                                           C; 518
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                                                                                                                           U; 0 Other;
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RESULT 13
ADI61666/c
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                                       RESULT 14
AEA43831/c
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AXU
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                                                                                                                                                                                                               Query Match
Best Local S
Matches 84
AEA43831;
                                                                                                                                                                                                                                                                                                The invention relates to a new composition comprising ADI61633-ADI61770and their complements that are cDNAs differentially expressed in brain disorders. Also included are a high throughput method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids and a high throughput method for screening a library of molecules or compounds to identify a ligand that specifically binds a cDNA. The expression of the each of the CDNAs is downregulated at least two-fold in the brain of the subjects with Alzheimer's disease (ADI61727) or upregulated at least two-fold in Alzheimer's disease (ADI61727). The composition is useful for diagnosing or treating Alzheimer's disease. The present sequence is a cDNA downregulated at least two-fold in the brain of the subjects with Alzheimer's disease.
                                                                                                                                                                                                                                                                          Sequence
                         AEA43831 standard; cDNA; 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising cDNAs that are differentially expressed in brain disorders, useful for diagnosing or treating Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-118572/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-2000; 2000US-00566921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA downregulated in Alzheimer's disease, INCYTE 413797.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI61666 standard; cDNA; 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-2000; 2000US-00566921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 88; Alzheimer's disease; differential display; neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-2004 (first entry)
                                                                                                                                                     686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder.
                                                                                                                                                                                                                   84.
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                         2677
                                                                                                 ATTACTTCCTTGTAGATAAGTTCTTT 1710
                                                                                                                  ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 34; 223pp; English
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                         BP; 785 A; 598 C; 581
                                                                                                                                                                                                                             10.3%;
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                                                                                                                                                                                                                0,
                                                                                                                                                                                                                              Score 82.8; DB 12
Pred. No. 6.8e-09;
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                         G;
                                                                                                                                                                                                                                                                         712 T; 0 U; 1 Other;
                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                                                            Length 2677
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Query Match

Local

Similarity

10.3%; ð

Score 82.8; Pred. No. 6.

Length 2677; Indels

0

Gape

0

0

Mismatches

BP;

Ç 581

G.

712 T; 0 U; DB 14;

1 Other;

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CR treatment or for the monitoring of treatment of a subject with a brain of disorder. (I) comprises several cDNAs that are differentially expressed con in brain disorders and chosen from any one of 138 nucleotide sequences of CARA3798-ARA43935, or thair complements. Also described: (1) a high collaboration and sample containing nucleic acids; (2) an isolated cDNA (II) collaboration and ambiguity method for detecting differential expression of one or more collaboration and activation of one or more collaboration and activation composition vector (III) containing (III); (2) a high composition vector (III) containing (III); (3) an expression of one or more composition and (6) a pharmaceutical composition composition (V) produced using (IV); and (6) a pharmaceutical composition composition (V); (I) is useful compounds to identify a ligand which specifically binds a cDNA, where the compounds to identify a ligand which specifically binds a cDNA, where the method involves combining (I) with the library of molecules or compound (IV) is useful for culture. (V) is useful for bind throughput method for screening a library of molecules or compounds to identify a ligand which specific binding the protein from the culture. (V) is useful for bind throughput method for screening a library of molecules or compound under conditions to allow specific binding throughput method for screening a library of molecules or compound under conditions to allow specific binding the protein from the culturation of the protein partition with the sample under conditions to compound. (V) is useful for purifying a ligand from a sample, which involves combining (V) or its portion with the sample under conditions to compound to compound the protein from the protein from the protein from the protein and separating the condition and another conditions to condition from ligand. (V) or its portion with the sample under conditions to condition from ligand. (V) or its portion with the sample under conditions to condition to condition to condition to con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; treatment; brain disease; neuroprotective; cerebrop muscular-gen.; cycostatic; neuroleptic; nootropic; antidepress anticonvulsant; analgesic; antiparkinsonian; ophthalmological; immunotherapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition useful for diagnosis, staging, treating or monitoring treatment of a subject with a brain disorder, comprises several cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 34; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that are differentially expressed in brain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-456990/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA differentially expressed in brain tissue SEQ ID NO:34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ve; cerebroprotective;
antidepressant;
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RESULT 15
AEG09275/c
ID AEG092
XX AE
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This invention describes a novel method of identifying a compound that inhibite the processing of amyloid-beta precursor protein in a mammalian cell. The invention also describes; a) an agent for inhibiting amyloid-beta precursor processing consisting of an antisense polynucleotide, a ribozyme or a small interfering RNA (siRNA), where the agent comprises a nucleic acid sequence complementary to, or engineered from, a naturally-coccurring polynucleotide sequence encoding the polypeptide comprising the amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical composition comprising the agent for inhibiting amyloid-beta precursor processing or an amyloid-beta precursor processing or inhibiting amount of mitogen activated protein-kinase inhibitor in admixture with a carrier. The method involves activation of a biological pathway producing an indicator of the processing of amyloid-beta precursor protein e.g. a phosphorylated substrate of a kinase comprising AEG09268-AEG09268. The indicator induces the expression of a reporter e.g. alkaline phosphatase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound that inhibits amyloid-beta precursor protein processing in a mammalian cell for treating e.g., Alzheimer's disease by measuring a compound-polypeptide property related to amyloid-beta peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2006-231019/24.
P-PSDB; AEG09284.
REFSEQ; NM_138980.
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mitogen activated protein-kinase inhibitor; neurological disease;
Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spittaels KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-2004; 2004US-0570352P.
24-AUG-2004; 2004US-0603948P.
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LAENEN W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 669. .1949
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transcript variant 3"
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Best Local
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                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, use diagnostics, forensics, gene mapping, identification of mapping that is and to responsible for genetic disorders or other traits and to
                                                                                                                                                                                                          WPI; 2001-639362/73.
P-PSDB; ABG29395.
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2698 BP;
                                                                                                                 Claim 1; SEQ ID NO 29386; 103pp; English
                                                                                                                                           biodiversity.
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o assess
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a

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RESULT 17
AAS66964/C
ID AAS669
XX AAS669
XX DAS669
XX DNA en
XX Human;
KW Human;
KW Homo 8
XX Homo 1
XX Ho
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Best Local S
Matches 81
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P-PSDB;
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in retating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodivérsity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, use diagnostics, forensics, gene mapping, identification of n responsible for genetic disorders or other traits and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631
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DB; ABG02777.
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Pred. No. 1
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diagnostic; genetic disorder;
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RESULT 18
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Best Local S
Matches 81
                                                                                           diagnostics, for responsible for biodiversity.
                                                                                                       New isolated polynucleotide and encoded polypeptides, undiagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and treesponsible for genetic disorders.
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23-AUG-2000; 2000US-00649167
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DB; ABG11497.
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upplement; medical imaging; diagnostic; genetic of

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                                                                                                                                                                                                        RT, Liu C,
                                                                                                                                                                                                                                    HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel
                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 221 A; 277 C; 313 G; 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 1111
                                                                                                                                                                                                      Tang
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                                                               103pp;
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                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                         disorder;
                                                                                                                       mutations
                                                                                                                                                                                                                                                                                                                                                                                                                         88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
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sequences. (I) reaction (PCR) and in recombin

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used

relates) is useful as ny... anu ...
rimers, oligomers, anu ....
rimor of (II). 7

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RESULT 19
AAA59379/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc in diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal cc activity of (II) or to treat disease states involving (II). (II) is consisted the sequence involving (II) and its antibodies against it, detecting or quantitating a colypeptide in tissue, as molecular weight markers and as a food cc polypeptide in tissue, as molecular weight markers and as a food complement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cand to produce other types of data and products dependent on the analysis of the invention. Note: The sequence data for this coding sequences of the invention. Note: The sequence data for this coding the product of the invention of the product of the produc
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JNK3; c-jun N-terminal kinase 3; JNK3alphal isoform; JNK3alpha2 isoform; mitogen-activated kinase; neurodegeneration; apoptosis; neuron; neurodegeneration; at a fain injuty; neurodegeneration; at a fain injuty; Huntington's disease; aging; acquired immune deficiency syndrome;
                   WPI; 2000-499230/44.
P-PSDB; AAB07788.
                                                                                                                                                                                 20-JAN-1999;
26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding
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                                                                                    Desanlis F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                   (AVET ) AVENTIS PHARMA SA
                                                                                                                                                                                                                                                                                                                                              NO200043524-A1
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                                                                                       Fournier
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                                                                                                                                                                                 99FR-00000586.
99US-0122175P.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            /product= "JNK3deltaNalphal'
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                                                                                       Maury
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                                                                                    Zhou-Liu
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RESULT 20
ABL88411/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes derivatives of JNK (c-jun N-terminal kinase) 3, which have deletions from the N-terminal region corresponding to positions 1-38 of the JNK3alphal and alpha2 isoforms or a C-terminal deletion from position 139. JNK are mitogen-activated kinases implicated in neurodegeneration and apoptosis of neurons. The derivatives are used to identify specific ligands. These ligands, and JNK3-specific antibodies, are used for prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's, Parkinson's or Huntington's diseases, degeneration associated with aging or acquired immune deficiency syndrome, brain injury, or cerebral anoxia, hypoxia or edema. Vector containing sequences encoding the derivatives are useful in gene therapy, e.g. of spinal cord injury and retinal degeneration. The present sequence encodes the derivative JNK3deltaNalphal
                                       Claim 1; Fig 34; 213pp; German
                                                                                Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific peptides
                                                                                                                              P-PSDB; ABB85006.
                                                                                                                                           WPI; 2002-257469/30.
                                                                                                                                                                                                                                03-AUG-2000; 2000DE-01037759
                                                                                                                                                                                                                                                             03-AUG-2001; 2001WO-EP009011
                                                                                                                                                                                                                                                                                         14-FEB-2002
                                                                                                                                                                                                                                                                                                                    WO200212338-A2
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                           Pain; analgesic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1306 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Pain regulated cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          known isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New derivatives of c-jun N-terminal kinase 3, useful for identifying ligands for treatment of neurodegeneration, have specific deletions
                                                                                                                                                                                                     (CHEF ) GRUENENTHAL GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; cDNA; 1773 BP
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                                                                                                                                                                        Wetzels I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                              disease; gene;
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                                                                                                                                                                        Wnendt
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The invention comprises (i)

relates to identifying pain-regulating substances incubating a test substance with a cell (or prepar

preparation

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RESULT 21
AED32365/c
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Best Local
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The invention relates to a novel differentiation inducing agent of a leukemia cell. The agent comprises an expression activator or functional activator of a promyelocytic leukemia (PML) protein, or an expression inhibitor or functional inhibitor of the PMLK protein (a PML specific
                                                                                                       Differentiation inducing agent of leukemia cell useful as leukemia therapeutic agent, comprises expression activator/functional activa promyelocytic leukemia protein, or expression inhibitor/functional inhibitor of PMLK protein.
                                                                                                                                                                                                                                                                                                                                                                                                     JP2005281183-A.
                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                 Kitabayashi K,
                                                                                                                                                                                                                                                                                                          29-MAR-2004; 2004JP-00097088.
                                                                                                                                                                                                                                                                                                                                       29-MAR-2004; 2004JP-00097088
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                                                                                                                                                                                                                                                               (DOKU-)
                                                                                                                                                                                                                                                                              (KOKU-)
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                                                                                                                                                                                     2005-717904/74.
)B; AED32366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promyelocytic leukemia
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                                                                                                                                                                                                                                                          KOKURITSU GAN CENT SOCHO.

DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                             OES
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                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human promyelocytic leukemia protein kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
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Pred. No. 2.2e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase encoding gene,
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Best Local
                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes, (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to represent the sequence of the seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, u diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and tresponsible
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23-AUG-2000;
                                  involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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supplement; medical in
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Pred. No. 2.2e-08;
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RESULT 23
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Best Local :
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                                                             Identifying a compound that inhibits amyloid-beta precursor protein processing in a mammalian cell for treating e.g., Alzheimer's disease by measuring a compound-polypeptide property related to amyloid-beta peptide
                                                                                                               WPI; 2006-231019/24
P-PSDB; AEG09285.
REFSEQ; NM_138981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amyloid-beta precursor protein; pharmaceutical; mitogen activated protein-kinase inhibitor; neurological disease; halzheimer's disease; depeneration; cognitive disorder; Neuroprotective; Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
                       Example 1; SEQ ID NO 12; 84pp; English
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24-AUG-2004; 2004US-0603948P.
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Pred. No. 2.2e-08;
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This invention describes a novel method of identifying

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitogen activated protein-kinase inhibitor in admixture with a carrier. CC The method involves activation of a biological pathway producing an CC indicator of the processing of amyloid-beta precursor protein e.g. a CC phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The CC indicator induces the expression of a reporter e.g. alkaline phosphatase, CC GFP, eGFP, dGFP, luciferase or beta-galactosidase in the mammalian cell. CC The pharmaceutical composition further comprises a label indicating use CC cognitive impairment or a susceptibility to the condition. The agent is CC cognitive impairment or a susceptibility to the condition for cessing or preventing a condition from or comprise of amyloid-beta precursor protein in a subject suffering from or compressing or preventing a condition involving cognitive impairment or a susceptibility to the condition, preferably, Alzheimer's disease. This sequence encodes thuman mitogen-activated protein kinase 10 (MAPKIO), transcript variant 4, a kinase involved in the up-regulation of amyloid-beta 1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                      C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; Alzheimer's disease; Huntington disease; amyotrophic lateral ischemia; trauma; motorneuron disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence encoding the polypeptide comprising the amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical composition comprising the agent for inhibiting amyloid-beta precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell. The invention also describes; a) an agent for inhibiting emylo beta precursor processing consisting of an antisense polynucleotide, ribozyme or a small interfering RNA (siRNA), where the agent comprise
                                           Davis RJ,
                                                                                                           03-OCT-1997;
                                                                                                                                            05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                    Seq ID No: 6 of WO9918193
                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2003
21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX37276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX37276 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2155 BP;
             WPI; 1999-287734/27
                                                                                                                                                                            15-APR-1999
                                                                                                                                                                                                        WO9918193-A1
                                                                                                                                                                                                                                                                        human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        processing or an amyloid-beta precursor processing-inhibiting
                                                                           (UYMA-) UNIV
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibits the processing of amyloid-beta precursor protein in a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCCTTGTAGATAAGTTCTTT 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCTTGTAGATAAGTTCTGT 711
                                             Flavell RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first en
                                                                             MASSACHUSETTS
                                                                                                           97US-0060995P
                                                                                                                                            98WO-US020904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 A; 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2372
                                               Rakic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80.4; D
Pred. No. 2.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 446 G;
                                               שי
                                               Whitmarsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3e-08;
les 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15;
                                               £,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for inhibiting amyloid-
                                                Kuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2155;
                                               Ç
                                               Yang
                                                                                                                                                                                                                                                                                                                         disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises
                                                                                                                                                                                                                                                                                                            sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amount
                                               Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Identification of c-Jun N-terminal kinase 3 modulators.

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RESULT 25
AAL48611/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method CC comprises (a) incubating a cell that can express a JNK3 protein, or that CC has JNK3 activity, with a compound under conditions and for a time CC sufficient for the cell to express a JNK3 protein/activity without the compound; (b) incubating a control cell under the same conditions and for CC the same time without the compound; (c) measuring JNK3 expression/activity in the cell in the presence of the compound; (d) comparing the CC amount of JNK3 expression/activity in the presence and absence of the compound, where a difference in the level of expression/activity. The CC indicates that the compound modulates JNK3 expression/activity. The CC invention also provides a transgenic non-human mammal having a transgene CC disrupting expression of a JNK3 gene, the transgene being chromosomially CC e.g. antisense nucleic acids, are used to treat disorders involving CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, Parkindon's CC disease or epilepsy. JNK3 sequences under GenBank accession numbers CC U34819, U34820, U07620, L27128, L35236, X12740 and V00727 can be used in CC field.)
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Best Local
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                                    12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                          12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                          ISM;
                                                                                                                                                                                                                                                                                                                                                                                                                          AAL48611 standard; cDNA; 2372
                                                                                                                                                                      11-JAN-2002;
                                                                                                                                                                                                                              WO200255664-A2
                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                  Human insulin receptor signaling modifier cDNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0 U; 0 Other;
                                                                                                               12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1475
                                                                                                                                                                                                                                                                                          diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630
                                                                                                                                                                                                                                                                                                     insulin receptor signaling; insulin receptor signaling modifier;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCCTTGTAGATAAGTTCTTT
                                    2001US-0261226P.
2001US-0261303P.
2001US-0261335P.
2001US-0261336P.
2001US-0261336P.
2001US-0261456P.
2001US-0261457P.
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                       2002WO-US001048
          2001US-0261458P.
2001US-0261459P.
                                                                                                                                                                                                                                                                                       metabolic syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2D; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80.4; DB 2;
Pred. No. 2.3e-08;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711
                                                                                                                                                                                                                                                                                     antidiabetic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                 Query Match
Best Local S
Matches 81
                                                                                                                                                                                                                             The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent -biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM coding sequence described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                   Sequence 2372 BP; 714 A; 548 C; 519 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 39-41; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-599664/64.
P-PSDB; AAO18492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seidel-Dugan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EXEL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L2-JAN-2001;
1415
                                 690
                                                                                     630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTTCTTCTGAATTCATTA
                                                                                                                                  81;
                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXELIXIS
CTTCCTTGTAGATAAGTTCTTT 1394
                   CTTCCTTGTAGATAAGTTCTGT 711
                                                                  CTGAAGGAGAAGGCTGTCCTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2001US-026151BP
2001US-0261531P
; 2001US-0261532P
; 2001US-0261589P
; 2001US-0261590P
; 2001US-0261694P
; 2001US-0261695P
; 2001US-0261697P
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferguson
                                                                                                                                                10.1%;
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                                                                                                                                 0,
                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidd
                                                                                                                                  Mismatches
                                                                                                                                                80.4; DB 6;
No. 2.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                   591 T; 0 U; 0 Other;
                                                                                                                                                                  9
                                                                                                                                                                Length 2372;
                                                                                                                                  Indels
                                                                                                                                 ç,
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                   agent
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RESULT 26
ACA56791/c
30-JAN-1998;
                 31-DEC-2002.
                                                                                Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma
                                    US6500938-B1
                                                                                                          Human signalling pathway polynucleotide probe
                                                                                                                              06-JUN-2003
                                                                                                                                                 ACA56791;
                                                                                                                                                                   ACA56791 standard;
                                                     Homo sapiens
                                                                       .mmunopathy;
                                                                        AIDS;
                                                                                                                              (first entry)
98US-00016434.
                                                                        asthma; neuropathy;
                                                                                                                                                                    CDNA;
                                                                        Alzheimer'
                                                                                  adenocarcinoma; leukaemia;
                                                                                                            SEQ
                                                                                                             Ħ
                                                                        disease; microarray
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                                                                                                            1389
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RESULT 27
ADI56587/c
ID ADI565
XX BUMAN
DE Human;
XX Human;
XX Buman;
XX Buman;
XX Grug d
XX Bignal
XX Giabet
XX diabet
XX Giabet
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XX Homo &
XX
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Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discovery and development, toxicological and carcingenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alreimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic forms at directly from USPTO at
                                                           drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland, bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropat dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug
                                                                                                                                                                Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                       Homo sapiens
                                                                                                                                                                                                                            Human polynucleotide probe #1389
                                                                                                                                                                                                                                                                       22-APR-2004
                                                                                                                                                                                                                                                                                                                ADI56587
                                                                                                                                                                                                                                                                                                                                                        ADI56587 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAAITCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCTTGTAGATAAGTTCTTT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1389; 65pp; English
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seilhamer JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 714 A; 548
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 519 G; 591 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGTCTTTTCTTCTGAATTCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 Other;
                                                                                 neuropathology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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26-AUG-2004 ADP45599

(first entry

ADP45599 standard; cDNA; 2372 BP

Human MAP

kinase MAPK10 (JNK3)

CDNA

breast cancer; cytostatic; gene therapy; human; ss; single nucleotide polymorphism; MAP kinase; MAPK10;

gene;

SNP; JNK3A; p493F12;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes CC comprising at least a portion of a gene encoding at least a portion of gene encoding at transducing CC polypeptide and third polynucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the CC composition are useful as array elements in a microarray for monitoring CC the expression of target polynucleotides. The microarray for monitoring CC diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, CC microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway CC polypeptides. The composition can also be used to purify a subpopulation CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone marrow, brain, breast or cervix, CC unimmunopathology, e.g. Alzheimer's disease or depression. This sequence data for this patent did not form part of the printed specification but was contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2372 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID NO 1389; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-090520/09
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                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                  CTTCCTTGTAGATAAGTTCTTT 1394
                                                             CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           714 A; 548 C; 519
                                                                                                                                                                                                                                                                                                      10.1%;
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Pred. No. 2
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RESULT 29
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        of breast cancer comprising detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The method of the invention has cytostatic applications and may be useful for identifying a subject at risk of breast cancer, for early diagnosis, prevention and treatment of breast cancer, possibly via gene therapy, as well as to analyse and predict a response to a breast cancer treatment and in clinical drug trials. The current sequence is that of the human MAP kinase MAPK10 (JNK3, JNK3A; p493F12;p54bSAPK MAP kinase;c-Jun kinase 3;JNK3 alpha protein kinase;c-Jun N-terminal kinase 3;Stress activated protein kinase beta) cDNA of the protein which has been manned to be protein kinase beta) cDNA of the protein which has been manned to be protein kinase beta) cDNA of the protein kinase beta concerns and the protein kinase beta) cDNA of the protein kinase beta) cDNA of the protein kinase beta) cDNA of the protein kinase beta concerns and the protein kinase beta) cDNA of the protein kinase beta) cDNA of the protein kinase beta beta protein kinase beta beta protein kinase beta protein kinase beta beta protein kinase beta protein kinase prot
 cytostatic; gene therapy; human;
                              Mitogen-activated protein kinase
                                                                02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
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                                                                                                                              ADS92938 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a subject at risk of breast cancer by detecting the presence of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUMA1 or GALE regions which are associated with breast cancer in a nucleic acid sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for identifying a subject at
                                                                                                                                                                                                                                                                                                                                                                                                                                             invention which has been mapped to chromosomal position 4q22.1-q23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-2002; 2002US-0429136P
24-JUL-2003; 2003US-0490234P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SEQU-) SEQUENOM INC.
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                                                                                                                                                                                                                                    CTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                               CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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                                                                                                                                                                                                                CTTCCTTGTAGATAAGTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 9;
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224. .1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human MAP kinase MAPK10 (JNK3) protein"
                                                                                                                               CDNA;
                                                                entry)
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Pred. No. 2.3e
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acid sample
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Query Match
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                                                                                                                                                                                                                                                                                                                                    The invention describes a method of identifying a candidate branching morphogenesis modulating (MBM) agent. The method comprises: providing an assay system comprising a MBM polypeptide or nucleic acid; contacting the assay system with a test agent under conditions where the system provides a reference activity, except for the presence of the test agent; and detecting a test agent blased activity of the assay system, where a difference between the test agent as a candidate branching morphogenesis modulating agent. Also described are: a method of modulating branching morphogenesis in a mammalian cell; and a method for diagnosing a disease in a patient. The method is useful in identifying a candidate branching morphogenesis modulating agent for preparing a composition for diagnosing or treating cancer. This sequence encodes a human branching morphogenesis
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a candidate branching morphogenesis modulating agent treating cancer comprises contacting the assay system comprising polypeptide or nucleic acid with a test agent and detecting a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plowman GD, Karim FD, Swimmer C, Schulte-Merker S, Langheinrich U, Odenthal JH, Scheel JK, Will TT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; SEQ ID NO 9; 179pp; English
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30-DEC-2002;
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1415
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DB; ADS92969.
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                                                                                     CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
CTTCCTTGTAGATAAGTTCTTT 1394
                                                                                                                                   CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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                                                                                                                                                                                  Conservative
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2002US-0436941P
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                                                                                                                                                                                                     Score 80.4;
Pred. No. 2.
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SNP detection; breast tumor; endocrine disease;
gynecology and obstetrics; neoplasm; cytostatic; metastasis;

Human mitogen-activated protein kinase 10 (MAPK10)

CDNA

(first

entry)

ADX98578

ADX98578 standard; cDNA; 2372

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AEG09273
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Matches 81
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Key
                                                           amyloid-beta precursor protein; pharmaceutical; murological disease; mitogen activated protein-kinase inhibitor; neurological disease; Alzheimer's disease; degeneration; cognitive disorder; Neuroprote Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2003; 2003US-0490234P.
25-NOV-2003; 2003US-00723681.
25-NOV-2003; 2003US-0525239P.
                                                                                                                             Human MAPK10,
                                                                                                                                                     20-APR-2006
                                                                                                                                                                                                       AEG09273 standard; DNA; 2372
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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mitogen-activated protein kinase 10; Jun N terminal kinase-3; NAPK10
                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; SEQ ID NO 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide sequences within the human genome
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phtson CR;
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                                                                                                                          transcript variant 1 DNA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      10.1%;
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                                                                                                                                                                                                        BP
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                                                             Neuroprotective;
10; MAPK10; ds;
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This invention describes a novel method of identifying a compound that CC inhibits the processing of amyloid-beta precursor protein in a mammalian Cc cell. The invention also describes; a) an agent for inhibiting amyloid-beta precursor processing consisting of an antisense polynucleotide, a CC ribozyme or a small interfering RNA (sinNA), where the agent comprises a CC nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence encoding the polypeptide comprising the composition comprising the agent for inhibiting amyloid-beta precursor processing or an amyloid-beta precursor processing-inhibiting amount of a mitogen activated protein kinase inhibitor in admixture with a carrier. CC midicator of the processing of amyloid-beta precursor protein e.g. a cc indicator of the processing of amyloid-beta precursor protein e.g. a cc indicator induces the expression of a reporter e.g. alkaline phosphatase, CC GFP, eGFP, dGFP, luciferase or beta-galactosidase in the mammalian cell. CT he pharmaceutical composition further comprises a label indicating use of the composition for treating or preventing a condition. The agent is cuscipilible to the abnormal processing of the protein, or for treating or preventing a condition involving of amyloid-beta precursor protein in a subject suffering from or cusceptible to the abnormal processing of the protein, or for treating or preventing a condition preferably, Alzheimer's disease. This sequence encodes comparison the up-regulation of amyloid-beta involved in the up-regulation of amyloi
                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a compound that inhibits amyloid-beta precursor protein processing in a mammalian cell for treating e.g., Alzheimer's disease by measuring a compound-polypeptide property related to amyloid-beta peptide
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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24-AUG-2004; 2004US-0603948P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFSEQ; NM_002753.
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CTTCCTTGTAGATAAGTTCTTT 1394
                                     CTTCCTTGTAGATAAGTTCTGT 711
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/product= "mitogen-activated protein kinase 10
transcript variant 1"
                                                                                                                                                                                                                                                                                                                                                                                          714 A;
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Human dithp intracell

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Human; dithp; diagnow

KW cancer; cell prolife;

KW inflammatory disorde

KW neurological disorde

KW neurological disorde

KW cancer; cell prolife;

KW disease model; toxic

KW denetive tissue di

gene therapy; antise;

KW disease model; toxic

KW connective tissue di

Gene therapy; antise;

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KW concer; cell prolife

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KW neurological disorde

KW neurological disorders; neurolog

CC coroll type and to
The invention relates to novel human diagnostic and therapeutic CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded CC proteins (DITHF; ABR41136-ABR41812). The invention also relates to CC polynucleotide sequences at least 90% identical to the dithp cDNA CC sequences of the invention; recombinant vectors, host cells and CC transgenic organisms comprising a dithp nucleic acid sequence; the CC recombinant production of DITHP proteins; antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of CC detecting dithp nucleotide and protein sequences; methods of screening CC for compounds which specifically bind a DITHP protein; and methods of CC assessing the toxicity of test compounds using a dithp hybridisation CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the CC diagnosis of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, CC viral, fungal or parasitic infections; hormonal disorders; metabolic consorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP CC groteins can additionally be used in analysts of the proteome of a tissue or cell type and to induce antibodies. The dithp nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dufour GE, Hillman JL, Yu JY, Tuason O, Daughtery SC, Dam TC, Liu TF, Ngyen DA, Peralta CH, David MH, Lewis SA, Chen AJ, Flores V, Marwaha R, Lo A, Lan RY, Urash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; antisense therapy; genot disease model; toxicological testing; intracellular signalling; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human dithp intracellular signalling protein-encoding cDNA
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2001US-0291280P.
2001US-0291849P.
2001US-0299428P.
2001US-0299476P.
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2001US-0280067P.
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O, Yap PE, A
DA, Kleefeld
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Yap PE, Amshey SR;
Kleefeld Y, Gerstir
Panzer SR, Harris E
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RESULT 33
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                    The invention relates to a new composition comprising ADI61633-ADI6170and their complements that are cDNAs differentially expressed in brain disorders. Also included are a high throughput method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids and a high throughput method for screening a library of molecules or compounds to identify a ligand that specifically binds a cDNA. The expression of the each of the cDNAs is downregulated at least two-fold in the brain of the subjects with Alzheimer's disease (ADI61727) or upregulated at least two fold in Alzheimer's disease (ADI61728-ADI61770). The composition is useful for diagnosing or treating Alzheimer's disease. The present sequence is a cDNA downregulated at least rwo-fold in the brain of the subjects with Alzheimer's disease.
                                                                                                                                                                                                                                                                          New composition comprising cDNAs that are differentially expressed brain disorders, useful for diagnosing or treating Alzheimer's dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a dithp cDNA encoding a DITHP protein which has intracellular signalling activity. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 33; 223pp; English.
                                                                                                                                                                                                                                                                                                                                WPI; 2004-118572/12
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                                                                                                                                                                                                                                                                                                                                                               Tingley DW,
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RESULT 34
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The invention relates to a composition (I) for the diagnosis, stagifig, treatment or for the monitoring of treatment of a subject with a brain consorder. (I) comprises several cDNAs that are differentially expressed in brain disorders and chosen from any one of 138 nucleotide sequences of AEA43798-AEA43935, or their complements. Also described: (I) a high throughput method for detecting differential expression of one or more CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II) cells of the about cell (IV), and (AEA43812, AEA43813, AEA43831, AEA43831, AEA43831, AEA43831, AEA43831, AEA43831, AEA43831, AEA438356, AEA43833 and AEA43923; (3) an expression vector (III) containing (II); (C) and (G) a pharmaceutical composition comprising (V). (I) is useful for a high throughput method of screening a library of molecules or compounds to identify a ligand which specifically binds a cDNA, where the method involves combining allow specific binding and detecting specific binding containing (IV) under conditions for the expression of the protein and recovering the protein from the coulture. (V) is useful for producing a protein, which involves culturing (IV) under conditions for the expression of the protein and recovering the protein from the coulture. (V) is useful for binding and detecting allows for the expression of the protein and recovering the protein from the coulture. (V) is useful for of molecules or compounds to identify a ligand which specifically binds (V), where the method involves combining (V) or its portion with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful for diagnosis, staging, treating or monitoring treatment of a subject with a brain disorder, comprises several cDNAs that are differentially expressed in brain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 33; 231pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-2000; 2000US-00566921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscular-gen.; cytostatic; neuroleptic; nootropic; antidepressant;
anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA differentially expressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
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Pred. No. 2.4e-08;
0; Mismatches 1
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ARBSULT 35
AAH4704/c
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Best Local S
Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide for rapid isolation of candidate eukaryotic cell clones comprises a promoter, a test gene, an IRES sequence and a surface marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRES; internal
label protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-476284/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ICON-) ICONIX PHARM
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1510 CTTCCTTGTAGATAAGTTCTTT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou H;
                                                                                                                                                                                                                                                                                                                            32-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribosome initiation sequence; promoter; surface membrane protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of pFastFind-Jnk3 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.1%;
                                                                                                                                                                                                                                                                                                                            32pp; English.
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Pred. No. 2.4e-08;
0; Mismatches 1
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The invention relates to a polynucleotide (I) comprising: (a) a regulatable promoter; (b) a test gene; (c) an IRES sequence; and (d) a surface marker coding sequence comprising a secretion signal sequence, a detectable label protein and a membrane protein where expression of the test gene also results in expression of the surface marker. A method is provided for identifying a host cell that exhibits regulated expression of a test gene complex that comprises (a) providing more than one host cell; (b) inducing the promoter; and (c) selecting a host cell that displays the surface marker on its surface. (I), the host cell and the method are useful for the rapid isolation of candidate eukaryotic cell

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RESULT 36
AAT10640/c
ID AAT10640;
XX Stress aci
XX CA2148898:
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Best Local
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                                                                                                                              A cDNA clone (AAT10640) was obtd. that codes for rat proline-directed stress-activated protein kinase (SAPK) p54 beta-I (AAR89410). This cDNA, and others (see AAT10638-39 and AAT1041-42) coding for p54 alpha-I, alpha-II, beta-II and gamma (AAR89408-9 and AAR89411-12), were isolated from a rat brain cDNA library following PCR amplification using primers based on p54 tryptic peptides obt. from a cycloheximide-treated rat
                                                                                                                                                                                                                                                                                                                                                                 DNA encoding recombinant P54 stress activated protein kinase related antibodies, useful for treating inflammation, hypoxia
                                                                                                                                                                                                                                                                                              Claim 20; Page 44-45; 68pp; English
                                                                                                                                                                                                                                                                                                                                                 stress, and
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-106355/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation;
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    Conservative
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                                                                                          BP; 556 A; 506 C; 488 G; 425 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Avruch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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364. .1644
/*tag== a
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                     86.0%;
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98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                              screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heat stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Banerjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2329
  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                          Score 66.8;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80.4; DB 4;
Pred. No. 3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woodgett
  2.8e-05;
ches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ن</u>
                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2005 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JR;
                                        Length 1975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8749;
  Indels
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                      and
  Gaps
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GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTC

685

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1445

ATTACTTCCTTGTAGATGAGTTCTTT 1420

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ABL88414/c
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                                                                                 Query Match
Best Local S
Matches 74
                                                                                                                                                        The invention relates to identifying pain-regulating substances (A) comprises (i) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analyssic activity. (A) along with nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                    and
and
                                                                                                                                  Sequence 1975 BP;
                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 34; 213pp; German.
                                                                                                                                                                                                                                                                                                                                                                                Identifying pain-regulating com
and for diagnosis, by measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-257469/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gillen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2001; 2001WO-EP009011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000; 2000DE-01037759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200212338-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pain; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL88414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL88414 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulated
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                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         ABB85009
ATTACTTCCTTGTAGATAAGTTCTGT
                                  GCACCTGAAGGTGAGGGCTGGCCTTTGACTACGCCGTTCTTAGTCTTCTCTGAGTTC
                                                     GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTACTTCCTTGTAGATAAGTTCTGT
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; neurological
                                                                                                                                    556 A; '506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                             86.0%;
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                                                                                 Score 66.8; D
Pred. No. 2.8e
0; Mismatches
                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                 compounds, useful for treating chronic pain ring binding of compounds to specific peptides
                                                                                                                                    C; 488 G;
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         711
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                                                                                                                                  425 T; 0
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                                                                                             .8e-05;
                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schaefer
                                                                                                          6
                                                                                    12:
                                                                                                                                    U; 0 Other;
                                                                                                         Length 1975;
                                                                                    Indels
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                                                                                 Gaps
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RESULT 38
ABL88413/c
ID ABL884
                                                   RESULT 39
AAT10641/c
X4X4X8
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Best Local
                                                                                                                                                                Matches
                                                                                                                                                                                                                 The invention relates to identifying pain-regulating substances (A) comprises (i) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analgesic activity. (A) along with nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain; including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The
        26-APR-1996
                                           AAT10641
                                                                                                                                                                                                 Sequence 1240 BP; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
                         AAT10641;
                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 34; 213pp;
                                                                                                                                                                                                                                                                                                                                                                  and proteins
                                                                                                                                                                                                                                                                                                                                                                         Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific peptides
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-257469/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000DE-01037759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2001; 2001WO-EP009011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200212338-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pain; analgesic; gene therapy; neurological neurodegenerative disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL88413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL88413
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHEF ) GRUENENTHAL GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pain regulated cDNA sequence
                                                                                                                                                              Local Similarity
nes 72; Conserv
                                                                                         1141
                                                                                                                           1201
                                                                                                           690
                                                                                                                                              630
                                                                                                   CTTCCTTGTAGATAAGTTCTGT
                                                                                         CCTCCTTGTAGATAAGTTCTTT 1120
                                                                                                                           CTGAAGGCGAGGGCTTGGCCTTTGACTACGCCATTCTTAGTCTTCTCTCTGAGTTCATTA
                                            standard;
                                                                                                                                              CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; cDNA; 1240
                                                                                                                                                              8.2%;
ilarity 87.8%;
Conservative
       (first entry)
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                                            CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Wnendt
                                                                                                                                                                                                                                                                                                                                                 German.
                                                                                                                                                                                                   299
                                            1986
                                                                                                                                                              Score 66; DB
Pred. No. 3.8e
0; Mismatches
                                                                                                                                                                0
                                                                                                                                                                                                  C; 317
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                                            ВP
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                                                                                                          711
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                                                                                                                                                                                                  G.
                                                                                                                                                          265 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Schaefer MK;
                                                                                                                                                                                                 0 U;
                                                                                                                                                                                Length 1240;
                                                                                                                                                                Indels
                                                                                                                                                                                                  0 Other;
                                                                                                                                             CTGAATTCATTA
                                                                                                                                                                0,
                                                                                                                                                               Gaps
                                                                                                                             1142
                                                                                                                                              689
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                                                                     RESULT 40
AAT10642/c
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Query Match
Best Local
                                                                                                                                  Matches
                                                                                                                                                                                                                                  A CDNA clone (AAT10641) was obtd. that codes for rat proline-directed stress-activated protein kinase (SAPK) p54 beta-II (AAR89411). This cl and others (see AAT10638-40 and AAT10642) coding for p54 alpha-I, alpl II, beta-I and gamma (AAR89408-10 and AAR89412), were isolated from a brain cDNA library following PCR amplification using primers based on tryptic peptides obt. from a cycloheximide-treated rat
                                                                                                                                                                                                                                                                                                                                                                             DNA encoding recombinant P54 stress activated protein kinase related antibodies, useful for treating inflammation, hypoxia stress, and for drug screening.
                                                                                                                                                                                             Sequence 1986 BP; 559 A; 510 C; 488 G; 427 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stress activated protein kinase; SAPK; p54 inflammation; hypoxia; heat stress; ss.
                                                                                                                                                                                                                                tryptic
                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kyriakis JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA2148898-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP
(ONTA-) ONTARIO CANCER IN:
1447
                                                              1507
                                                                                               630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTT
                                                                                                                                                                                                                                                                                                                                                  21; Page 46-47; 68pp; English
                                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ф
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                                                                                                                                                  Similarity
                                                                                                                                                                                                                                peptides
                               CTTCCTTGTAGATAAGTTCTGT 711
 CTTCCTTGTAGATGAGTTCTTT 1426
                                                                CTGAAGGTGAGGGCTTGGCTTTGACTACGCCGTTCTTAGTCTTCTCTCTGAGTTCATTA
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Avruch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "base 1549 i
probably C or G"
e 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00240014.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1549
                                                                                                                                                                                                                                obt.
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/note= "base 1550
/note= "case or G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 364. .1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase
                                                                                                                                              8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banerjee
                                                                                                                               Score 64.4; DI
Pred. No. 9.7e
O; Mismatches
                                                                                                                                  0
                                                                                                                                                                                                                                cycloheximide-treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p54 beta-II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Woodgett JR;
                                                                                                                                                    .7e-05
                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the specification,
                                                                                                                                                                Length 1986;
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody;
                                                                                                     GAATTCATTA
                                                                                                                                  0
                                                                                                                                                                                                                                                  ed from a based on
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                   is cDNA,
alpha-
                                                                                                                                                                                                                                                                                                                                                                                                      heat
                                                                   1448
                                                                                                   689
                                                                                                                                                                                                                                                   p54
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Stress activated protein kinase

p54 gamma cDNA.

AAT10642; 26-APR-1996

(first entry)

AAT10642 standard;

CDNA; 1408

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RESULT 41
ABT09489/c
ID ABT094
XX ABT094
XX ABT094
XX O5-DEC
XX Phase-
XX Phase-
XX ART tus
XX Rat; t
KW drug d
XX Ratus
XX W02002
XX W02002
XX 29-AUG
XX 29-JAN
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                                                                                                                                                                                                                                                                                         Hest Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                Rat; toxicity study; rat toxic response gene; toxicological response; drug development; phase-1 rat CT gene; ds.
                                                                                                                                                                                                                                                                                                    A GUNA GIONE (AAT10642) was obtd. that codes for rat proline-directed stress-activated protein kinase (SAPK) p54 gamma (AAR89412). This gDNA, and others (see AAT10638-41) coding for p54 alpha-I, alpha-II, beta-I and beta-II (AAR89408-11), were isolated from a rat brain gDNA library following PCR amplification using primers based on p54 tryptic peptides obt. from a cycloheximide-treated rat
 29-JAN-2002; 2002WO-US002935.
                 29-AUG-2002
                                  WO200266682-A2
                                                                                          Phase-1
                                                                                                            05-DEC-2002
                                                                                                                            ABT09489;
                                                                                                                                             ABT09489 standard;
                                                                                                                                                                                                                                                                                       Sequence 1408 BP; 408 A; 310 C; 339 G; 351 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding recombinant P54 stress activated protein kinase - related antibodies, useful for treating inflammation, hypoxia attress, and for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-106355/12
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(ONTA-)
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Predicting the liver toxicity of an agent to an individual by using test expression profile with a set of reference expression profiles Predictive Model to determine whether the agent will reduce liver toxicity in the individual.
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                                                                                                                                                                        (PHAS-)
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Best Local
The present invention describes a method for predicting the liver toxicity in an individual to an agent. The method comprises: (a) obtaining a biological sample from the individual treated with the agent; (b) measuring the expression of one or more liver toxicity predictive genes in the sample; and (c) using the test expression profile with a set of reference expression profiles in a Predictive Model to determine whether the agent will induce liver toxicity in the individual. Also described: (1) predicting the liver toxicity of an agent using an in vitro system; (2) predicting the liver toxicity in a biological sample
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                                                                                                                                                                                                                                                                                                                                                                      Predicting the liver toxicity in an individual to an agent by
the expression of one or more liver toxicity predictive genes
sample from the individual treated with the agent.
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                                                                                                                                                                                                                                                                                                                                       programmable machine; (3) a computer program product for enabling a computer to perform Predictive Model analysis for liver toxicity on a biological sample from an individual, in vitro cell cultures or explants to an agent; (4) a computer system adopted to predict liver toxicity in a biological system from an individual, in vitro cell cultures or explants to an agent; (5) a computer program product for predicting liver toxicity from a test sample expression profile; (6) mining genes predictive of liver toxicity; (7) an integrated system for predicting liver toxicity; and (8) identifying one or more liver inflammation predictive genes. The method is useful for predicting the liver toxicity in an individual to an agent. The present sequence represents a liver toxicity predictive gene sequence that represents a 24 hour combo 3 gene, which is specifically
                                                                                                                                                                                                                                                                                     Sequence 580
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                                                                                                                                  CCTANAGGAGACGGCTGCCCTCTTATGACGCCATTCTTAGTTCGCTCCTCCAAATCCATG
                                                                                                                                                                      CCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATT
                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                     B₽;
                                                                                                                                                                                                                                                                                                                           exemplification of the present invention.
                                                                                                                                                                                                                                                                                     170 A; 129 C; 145
                                                                                                                                                                                                                              6.2%;
                                                                                                                                                                                                        Score 49.4; DI
Pred. No. 0.19
0; Mismatches
                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                     <u>ن</u>
                                                                                                                                                                                                                                                                                   125 T; 0 U;
                                                                                                                                                                                                                              .19;
                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                     11 Other;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agent via
                                                                                                                                                                                                            Gaps
                                                                                                                                    435
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ADR91158/c
ID ADR911
XX ADR911
AC ADR911
AC ADR911
DT 16-DEC
XX Spleer
XX Unider
XX Unider
XX Unider
XX Unider
XX IT-MAI
XX IT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spleen necrosis predictive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR91158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR91158 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004083402-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression; toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spleen; toxicity; lymphoid; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114.
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detecting the altered expression of genes in a toxic response of the spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348) or their complete complements. The invention further comprises: monitoring the treatment of compound toxicity in a sample; predicting the spleen toxicity in an individual to an agent; predicting the spleen toxicity of an agent using an in vitro system; a computer program product for predicting spleen toxicity from an expression profile of nucleic

responses species.

WPI; 2004-691048/67

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Kier L,

Derbel M,

Nolan T;

17-MAR-2003; 2003US-0455443P

(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC

Claim 1;

SEQ

ij

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114;

249pp;

English.

New composition comprises cDNAs useful for detecting altered expression of genes in a toxic response of the spleen or for predicting toxic responses to one or more agents including lymphoid tissue types or other

scide from a sample under test, bearing an encrypted training d

comprising a computer readable medium ata set, encrypted lists of genes sele

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RESULT 45
ADB63776/c
ID ADB637776/c
ID ADB637
XX ADB637
XX ADB637
XX Human;
XX Human;
XX Human;
XX Human;
XX eigna;
XX osteo;
XX osteo;
XX Sept CDS
FT CDS
F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bearing an encrypted training data set, encrypted lists of genes selected CC from the cDNAs, and a predictive model for causing a general purpose CC computer to predict the spleen toxicity of the sample based upon the CC training data set, the list of genes selected from the cDNAs, and the CC expression profile of nucleic acids from the sample; and an integrated CC system for predicting spleen toxicity, comprising means for measuring CC gene expression profiles of spleen predictive genes from samples exposed to the test agent and a computer system operably linked to the means that CC is capable of implementing a predictive model. The composition comprising CC cDNAs is useful for detecting altered expression of genes in a toxic cresponse of the spleen or for predicting toxic responses to one or more agents including lymphoid tissue types or other species. The predictive CC genes and models of the invention are useful for identifying and CC evaluating various in vitro systems that can be used to accurately predict in vivo toxicity. This polynucleotide sequence represents one of the genes predictive for spleen necrosis of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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signal
     WPI; 2003-450961/43
P-PSDB; ADB65746.
                                                                                                              Yamamoto
                                                                                                                                                                                                                                                                  05-NOV-2001;
25-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002; 2002EP-00007401
                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1308459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB63776 standard; cDNA; 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                           (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; gene; pharmaceutical; diagnostic; gene therapy;
regeneration; cell regeneration; membrane protein;
transduction related protein; transcription-related protein;
orosis; neurological disease; cancer; tumour.
                                                                                                                                      H
                                                                                                                                                                                        HELIX RES
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                                                                               J, Isono
Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATT 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTAAAGGAGACGGCTGCCCTCTTATGACGCCATTCTTAGTTCGCTCCTCCAAATCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTICCTTGTAGATAAGTTCTGT
                                                                                  Sugiyama T,
I, Isono Y,
Oshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                     2001JP-00379298
2002US-00350978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 389 ..694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Clone UTERU20065470 protein"
                                                                                                                                                                                        INST.
BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone UTERU20065470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 129 C; 145
                                                                                  Otsuka M,
                                                                                                                                      Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49.4;
Pred. No. 0.
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                                                                                                              Otsuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711
                                                                               Wakamatsu A, Sı
suka K, Nagai K,
Nagahari K, Mas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 125 T; 0 U; 11 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                        Masuho
                                                                                                                                    Sato H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                              æ
                                                                                                                                      Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                              Tamechika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435
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The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide CC of the polynucleotide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide CC expressible manner and an antisense polynucleotide. The binding CC expressible manner for synthesising the polynucleotide or as a probe CC is useful as a primer for synthesising the polynucleotide, or as a probe CC for detecting the polynucleotide. The polynucleotide CC for detecting the polynucleotide. The polynucleotide CC genes may be included in them, for developing a diagnostic marker or CC of gene therapy. The genes are involved in tissue and/or cell cC regeneration. Membrane proteins, signal transduction-related proteins, can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate CC the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence content is not represented in the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as targets of gene therapy.
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                     б
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                                                                                             Matches
1322
                      989
                                                                                            l Similarity
65; Conserv
                     ATTACTTCCTTGTAGATAAGTTCTGTAAGAAA 717
                                                         GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                              GCACCTAAAGGAGAGGGCTGCCCCCGTATAACTCCATT
ATAACTTCCTTATATATCAATTCTGTAAAAGA
                                                                                             Conservative
                                                                                             0
                                                                                           Score 48.8; DB Pred. No. 0.35; 0; Mismatches
                                                                                             27;
                                                                                             Indels
                                                                                             0
                                                                                             Gaps
                                                                       685
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Query Match Best Local :

6.1%; 70.7%;

80

10;

Length

Local

Sequence 2372 BP; 682 A; 440 C; 486 G; 764 T; 0 U; 0 Other;

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RESULT
                                                                                                                                                                                                                   c-Jun N-terminal kinase; cytostatic; immunosuppressive; dermatological; antiinflammatory; cardiant; antirheumatic; antiarthritic; anti-HIV; respiratory-Gen; antipsoriatic; vasotropic; antibacterial; antilipaemic; cancer; colon cancer; renal cell carcinoma; prostate cancer; colon cancer; renal cell carcinoma; prostate cancer;
                                                                                                                                                   non-small cell carcinoma; psoriasis; pemphigus vulgaris; Behcet's syndrome; acute respiratory distress syndrome; ARDS; Behcet's syndrome; post-dialysis syndrome; leukaemia; ischaemic heart disease; post-dialysis syndrome; leukaemia; rheumatoid arthritis; AIDS; vasculitis; septic shock; inflammation;
                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                          DNA sequence encoding JNK2 protein.
                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                 ADJ64020
                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ64020 standard; DNA; 1765
                                                                                                                                     lipid histiocytosis;
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                               59. .1333
              /product=
                                /*tag=
                                                                 Location/Qualifiers
                                                                                                                                     JNK;
              "JNK2 protein"
                                                                                                                                      ds.
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RESULT 47
AAQ85309/c
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                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                            as colon cancer, renal cell carcinoma, prostate cancer, and non-small cell carcinoma, and non-malignant or immunological-related cell proliferative diseases, such as psoriasis, pemphigus vulgaris, Behcèt's syndrome, acute respiratory distress syndrome (ARDS), isothaemic heart disease, post-dialysis syndrome, leukaemia, rheumatoid arthritis, AIDS, vasculitis, septic shock, and other types of inflammation or lipid histiocytosis. The polypeptide of the invention may be useful in a screening method for identifying molecules which modulate its activity which are potentially useful as therapeutics. The present sequence represents a DNA sequence encoding the JNK2 protein used in the
                                                         AAQ85309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel polynucleotide encoding a c-Jun N-terminal kinase that phosphorylates the c-Jun N-terminal activation domain. The polynucleotide sequence of the invention may have cytostatic, immunosuppressive, dermatological, antiinflammatory, cardiant, antitheumatic, antipsemic, antipsemic, antipseed in the vasotropic, antipacterial, antilipaemic activities. Also disclosed in the invention are modulators of the activity or expression of the c-Jun N-terminal antilipsemic activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding a c-Jun N-terminal kinase (JNK), and the encoded polypeptide, useful for (identifying compounds for) treating cancer, psoriasis, rheumatoid arthritis, or septic shock.
25-MAR-2003
                            AAQ85309;
                                                                                                                                                                                                                                                                                                                        Sequence 1765 BP; 539
                                                                                                                                                                                                                                                                                                                                                       exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminal kinase (JNK) such as competitive inhibitor peptides, antiboc and sense or antisense polynucleotides which are useful for treating proliferative disorders associated with JNK. These include cancers is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KARI/)
(HIBI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Karin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1998
14-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-1994;
19-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3-FEB-1997
                                                                                                                                     1136
                                                                                                                                                                                                  1196
                                                                                                                                                                   069
                                                                                                                                                                                                                                630
                                                                                                                                                                                                                                                             61;
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HIBI M.
LIN A.
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ64021.
                                                         standard; DNA; 1780
                                                                                                                                                                                                                     CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
                                                                                                                                     CTTCTTTGTAAATTAGCTCTTT 1115
                                                                                                                                                                                                  SEQ ID NO 17; 50pp; English
                                                                                                                                                          CTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hibi M,
                                                                                                                                                                                                                                                             Conservative
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(revised)
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94US-00220602.
94US-00276860.
95US-00444393.
97US-00799913.
98US-00150201.
99US-00461649.
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                                                                                                                                                                                                                                                                          74.4%;
                                                                                                                                                                                                                                                                                                                       A; 356 C; 396 G;
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                                                                                                                                                                                                                                                          Score 48.4; DB Pred. No. 0.41; 0; Mismatches
                                                                                                                                                                                                                                                             0
                                                           ВP
                                                                                                                                                                   711
                                                                                                                                                                                                                                                                                                                       474 T;
                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                        0 Other;
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reating cell
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RESULT 48
ADA26313/c
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                                                                                                                                                                                                                                                                                       Matches 61;
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                             JNK1 (See AAR70767) and JNK2 phosphorylate the c-Jun N-terminal activation domain which affect gene expression from Ap-1 sites. The 2 protein kinases allow the detection of the level of specific kinase activity associated with activation of c-Jun and Ap-1. Cell proliferative disorders associated with JNK can be treated by administering a therapeutically effective amount of a reagent which modulates JNK activity. Disorders such as leukaemia, cancers of prostate, lung (nonsmall cell) and colon. (Updated on 25-MAR-2003 to correct PN field.)
immunological disorder; non-malignant cell-proliferative disorder;
leukaemia; organ related malignancy; acute inflammation;
c-Jun N-terminal kinase 2; JNK 2; immunopathological disorder;
                                               cDNA encoding
                                                                                                                                                                                                                                                                                                                                     Sequence 1780 BP; 541 A; 363 C; 402 G; 474 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onco:protein protein kinase, and gene expression in cells.
                                                                         20-NOV-2003
                                                                                                                          ADA26313 standard; cDNA; 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 57; Fig 28; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-075186/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1993;
25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cbs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncoprotein; polypeptide kinase; JNK; c-Jun; AP-1; leukaemia; prostate cancer; lung cancer; colon cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JNK2
                                                                                                  ADA26313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9503323-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC )
                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                        1196
                                                                                                                                                                                                              690
                                                                                                                                                                                                                                                                630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncoprotein polypeptide kinase coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIV CALIFORNIA.
UNIV MASSACHUSETTS MEDICAL SCHOOL
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR70768.
                                                                                                                                                                                                          CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                              CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
                                                                                                                                                                                      CTTCTTTGTAAATTAGCTCTTT 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis
                                                                                                                                                                                                                                                                                         Conservative
                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                c-Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-00094533
94US-00220602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R
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                                                                                                                                                                                                                                                                                                  6.0%;
74.4%;
                                                N-terminal kinase 2, JNK2
                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hibi M,
                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                       Score 48.4; DB Pred. No. 0.41; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JNK -
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                                                                                                                           ВÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for regulating c-Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derijard
                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                            , 2;
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                                                                                                                                                                                                                                                                                                                Length 1780;
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The invention relates to a method of treating an immunological disorder, con-malignant cell-proliferative disorder, leukaemia, an organ related malignancy or acute inflammation, associated with c-Jun N-terminal kinase (JNK), comprising administering to a subject, a compound which modulates the kinase activity. The method is useful for treating an immunological disorder, non-malignant cell-proliferative disorder, leukaemia, an organ related malignancy and acute inflammation. The disorder is associated with immunological disorder is an immunopathological disorder and is related to acute inflammation or septic shock, or the disorder and is related to acute inflammation or septic shock, or the disorder is acute respiratory distress syndrome (ARDS), AIDS or rheumatoid arthritis. The disorder associated with non-malignant cell-proliferative disorder is pooriasis, pemphigus vulgaris, ischaemic heart disease, leukaemia, post dialysis disorder and vascullitis. In organ related malignancy, the organ is the lymphoid system, breast, gastrointestinal system or genito-urinary tract. The present sequence represents cDNA encoding c-Jun N-terminal
                                                                                                                     Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1994;
18-JUL-1994;
19-MAY-1995;
13-FEB-1997;
08-SEP-1998;
14-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating immunological disorder, non-malignant cell-proliferative disorder, organ related malignancy or acute inflammation, associated co-Jun N-terminal kinase, by giving a compound which modulates kinase
                                                                                                                                                                               Sequence 1780 BP; 541 A; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 23; Page 32-34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KARI/)
(HIBI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           septid shock, acute respiratory distress syndrome, ARDS; AIDS; rheumatoid arthritis, psoriasis, pemphigus vulgaris; ischaemic heart disease; leukaemia; post dialysis disorder; ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002192218-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
                            690
                                                                                        630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-596275/56
                                                                                                                     l Similarity
61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KARIN M.
HIBI M.
LIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA26314.
                                                                           CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                            CTTCCTTGTAGATAAGTTCTGT 711
                                                        Hibi M,
                                                                                                                   6.0%;
ilarity 74.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-00861097
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94US-00220602
94US-00276860
95US-00444393
97US-00799913
98US-00150201
99US-00461649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease; leukaemia; post dialvais
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
59. .1333
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                 Score 48.4; D. Pred. No. 0.41 0; Mismatches
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                                                                                                                                                                               402
                                                                                                                                                                              G; 478 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         post dialysis disorder; vasculitis;
                                                                                                                                .41;
                                                                                                                                           9;
                                                                                                                     21;
                                                                                                                                                                              0 U;
                                                                                                                                              Length
                                                                                                                     Indels
                                                                                                                                                                              0 Other;
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                                                                                                                   Gaps
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á 밁 8

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Best Loc Matches Query Match

Local

Similarity

74.4%;

Conservative

0; Pred. No. Score 48.4;

Mismatches

.41; В 9, 21;

Length 1780; Indels

0

Gaps

0

Sequence 1780

BP;

541

A; 359 6.0%;

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RESULT 49
ACA62801/c
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18-JUL-1994;
19-MAY-1995;
13-FEB-1997;
08-SEP-1998;
                          which is useful for treating a cell proliferative disorder, where the effect is inhibition or stimulation of the kinase, and the composition in an immunosuppressing agent. The composition identified by the above method, is useful for treating a cell proliferative disorder e.g. cancer psoriasis, pemphigus vulgaris, Behcet's syndrome, acute respiratory distress syndrome (ARDS), ischaemic heart disease, leukaemia, rheumatoid arthritis, AIDS, vasculitis and septic shock. The present sequence represents the human c-Jun N-terminal kinase, JNK2, cDNA
                                                                                                                                           The invention relates to a method of identifying a composition useful treating a proliferative disorder, affecting a kinase having serine an threonine kinase activity and phosphorylating a c-Jun N-terminal activation domain. The method is useful for identifying a composition
                                                                                                                                                                                                                                                 Identifying a composition useful to treat a cell proliferative disorder, comprises incubating the composition and a serine/threonine kinase or polynucleotide encoding the kinase and measuring the effect of the composition on the kinase.
                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                         Karin
                                                                                                                                                                                                                                                                                                                                                                                                   (KARI/)
(HIBI/)
(LINA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      threonine kinase; psoriasis; pemphigus vulgaris; Behcet's syndrome; acute respiratory distress syndrome; ARDS; ischaemic heart disease; leukaemia; rheumatoid arthritis; AIDS; vasculitis; septic shock; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003044788-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c-Jun N-terminal kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human c-Jun
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                                                                                                                                                                                                                                                                                                                                                                         M, Hibi M,
                                                                                                                                                                                                                     3; Page 32-34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   KARIN M.
HIBI M.
LIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JNK2; cell proliferative disorder; serine kinase; ss; gene; ine kinase; psoriasis; pemphigus vulgaris; Behcet's syndrome; respiratory distress syndrome; ARDS; ischaemic heart disease;
                                                                                                                                                                                                                                                                                                                              ABU62138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-00861098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00220602.
94US-00276860.
95US-00444393.
97US-00799913.
98US-00150201.
99US-00461649.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "JNK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                         Lin
                                                                                                                                                                                                                                                                                                                                                                         P
C; 402
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 478 T; 0
 U; 0 Other;
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RESULT 50
AAA48656/C
ID AAA486
XX AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel method for modulating cell adhesion molecule expression involves antisense inhibition of a tumour necrosis factor (TNF) alpha signalling molecule. In the method TNF alpha signalling molecules Ha-ras, C-raf and C-Jun N-terminal kinase (JNK) 2 were inhibited by antisense oligonucleotides. In addition an antisense oligonucleotide to the cell adhesion molecule E-selectin was also examined. The present sequence is
                                                                                      contained modifications, namely phosphorothicate linkages and 2'methoxyethoxy bases. Some C residues also had a 5'methyl modification. Inhibitors of the TNF alpha signalling molecules have antibacterial, immunosuppressive, antipsoriatic, antidiabetic, antithyroid, cytostatic, dermatoological, antiallergic and antiinflammatory activity. The antisense inhibitors may be useful for the treatment of sepsis, rheumatoid arthritis, inflammatory, immune disease, inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; E-selectin; TNF alpha; cell adhesion; human; tumour necrosis factor alpha; phosphorothicate; methoxyethoxy; sepsis; rheumatoid arthritis; inflammatory; immune disease; inflammatory bowel disease; allergic contact dermatitis; psoriasis; inflammatory bowel disease; allergic contact dermatitis; psoriasis; inmunosuppressive; antipsoriatic; antidabetic; antithyroid; cytostatidermatological; antiallergic; Ha-ras; c-raf; c-Jun N-terminal kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating cell adhesion molecule expression for treating immune or inflammatory diseases involves treating cell with specific inhibitor of Tumor Necrosis Factor alpha signaling molecule.
                                                    allergic
                                                                                                                                                                                                                                                                                                                                                                                                                   oligonucleotide. The antisense oligonucleotides used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                      human JNK2 DNA. This sequence was also examined. The present sequence is human JNK2 DNA. This sequence was used to generate the JNK2 antisense olioonucleotide. The antisense olionomers of the sequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 88-90; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY94503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-2000
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Search completéd: July 19, 2006, 18:53:02 Job time : 658 secs

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AA663771 ae68h10.e
BM704479 UI.H-CK1-
BM50852 iii7a11.y
CK825957 ik36f03.y
GR25957 ik36f03.y
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BM945535 DA405335
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ORGANISM
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Email: mdaddms@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 401)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence. AQ046186
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RPCI11-31H10.TJ RPCI-11 Homo
                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
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                                                                                             AGGATTACTGAGCTCCACACTTGACTTGATGGTCAAAAGGGCATTATTGGCTCTGAATTTTG
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RPCI11 Human Male BAC Library"
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/db_xref="GDB:7511697"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                   source
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seatt Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3045 row: K column: 8 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ129390 393 bp DNA linear GSS 23-SEP-1998 HS_3045_A2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 COl=8 Row=K, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.

1 (Dases 1 to 393)
Mahairas,G.G., Wallace,J.C., Smith,K.,
Mahairas,G.S., Voune
Keller,A., Shaker,R., Furlong,J., Youne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10449764
                                          TGAATTTTGATGAGGCACATT-TACCCTTTAGCCCCATGTTAACATTTTCTTCAGGATTCA 389
                 TCATTTTGTATCAGGCACATTACTCCATATAGACCATGTTGACATATTGTTCAAGATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCC
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                                                                               36.6%;
ilarity 91.7%;
Conservative
                                                                                                                                                                                                                                                                                                                     quality sequence stop: 393.
Location/Qualifiers
                                                                                                                                                                /clone lib="CIT Approved Human Genomic Sperm Library D"/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3045 Col=8
                                                                                                                                                                                                                'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:3506556
                                                                             Score 293.2; DB 11
Pred. No. 1.3e-56;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wallace JC,
ncing Center
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                                                                                                                 DB 11;
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Swartzell,S., g,J., Zhao,S.,

Holzman,T., Adams,M.D.

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Gaps

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RESULT 3
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Best Local S
Matches 84
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PUBMED
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Tel: 216 431 9900
Fax: 216 361 9596
Fax: 779in@ather
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Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (bases 1 to 247)

1 (bases 1 to 247)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,

Cain, S., Leventhal, C., Costanzo, D., McElligott, K., Boozer, S.
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RST24016 Athersys RAGE Library
BG204609
BG204609.1 GI:13726296
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Scott J. Cain
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                     GTACCTGAAGGAGAAGGCTGTCCTTTTACACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATGTGATATTTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGCAACCCCTA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAATGAATGCCACAATGAATATCAGAAGAAATAGAACTAAAGTCATTATAAGGACACAA
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                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 197
Location/Qualifiers
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    scain@athersys.com
                                                                                                                                                               /clone lib="Atherrys RAGE Library"
/clone lib="Atherrys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                  xref="taxon:9606"
l_line="HT1080"
                                                                                          10.3%;
                                                                        Score 82.8; D
Pred. No. 2.8e
0; Mismatches
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S CDNA, mRNA sequence.
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VERSION
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                                                                                          Query Match 10.:
Best Local Similarity 97.'
Matches 84; Conservative
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BENDOCTINE PANCEAS CONSORTIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Other ESTs: is29b07.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Endocrine Pancress Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is29b07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6553861 5' similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: -40UP from Gibco
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.
1 (bases 1 to 390)
Melton, D., Brown, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                            GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                 /clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: NotI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Purified_pancreatic_islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6553861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                    10.3%;
                                                                                               0
                                                                                          Score 82.8; DB 4;
Pred. No. 2.9e-08;
0; Mismatches 2;
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ATTACTTCCTTGTAGATAAGTTCTGT

ATTACTTCCTTGTAGATAAGTTCTTT

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                                            AW297251/c
                                                                      RESULT 6
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                                                                                                                                        39
AW297251
UI-H-BW0-aji-b-12-0-UI.sl NCI_CGAP_Sub6 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A. F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-FT0202-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            021100-455-f02&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
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Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QV1-FT0202-021100-455-f02
BF856752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                              ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                            GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAATTC 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    +55-11-270700:
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: prostate tumor; Vector: puc18; Site 1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _xref="taxon:9606"
v_stage="Adult"
one_lib="FT0202"
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                                                                                                                                                                                                                                                                                                                                            10.3%;
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Pred. No. 2.9e-08;
                                                                                                                                                                                                                                                                                                                         Mismatches
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FT0202 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 (7),
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                                                                                                                                                                                                                                                                                                                                                                 Length 407;
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                                                                                                                                                                                                                                                                                                                       Gaps .
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FEATURES
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AUTHORS
TITLE
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SOURCE
                                                                                                                            ORIGIN
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Matches
                             Query Match
Best Local Similarity
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84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution CI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
I.M.A.G.E. Consortium/LNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 Forward POLYA=Yes.
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Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi:.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE:2731750 3', mRNA sequence
AW297251
AW297251.1 GI:6703887
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1 (bases 1 to 429)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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   Conservative
                                                                                                                                                                                                                                       /Clone lib="NAME 231.30"
/Clone lib="NCI CGAP Sub6"
/Clone lib="NCI CGAP Sub6"
/Clone lib="NCI CGAP Sub6"
/MCI CGAP Sub6 is a subtracted library derived from BW,
NCI CGAP Sub6 is a subtracted library derived from BW,
NCI CGAP Sub6 is a subtracted library derived from BW,
NCI CGAP Sub6 is a subtracted library derived from BW,
NCI CGAP Sub6 library had 7 million recombinants. A
Single-stranded DNA preparation of four normalized libraries:
NCI CGAP Sub6 library had 7 million recombinants. A
single-stranded DNA preparation of BW was used as a tracer
in a subtractive hybridization with a driver comprising:
the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM 3334-3337,
1456008-1456775,1500552-1502855); NCI CGAP Kid5 pool 1
LLAM 338-3342,3722-3725,
1233912-1325831,1471368-1472903,1492104-1493255);
NCI CGAP Lus pool 1 LLAM 3575-3582,3851-3584 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439); NCI CGAP GC4
pool 1 LLAM 3164-3167,3716-3720,3733-3735 (IMAGE
CloneIDs 1257096-1258631,146904-1470993,
1475592-1476743); NCI CGAP Pr22 pool 1 LLAM 2457-2459,
1101192-1101959, 1217928-1220615); NCI CGAP Sef010 pool 1
LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 986789,
1101192-1101959, 1217928-1220615); NCI CGAP GC4
population), plus a pool of 3,840 arrayed clones from
NCI CGAP Sub1 (IMAGE CloneIDs 2708616-2712455) and
NCI CGAP Sub2 (IMAGE CloneIDs 2712456-2723591) (30% of
the driver population), plus a pool of 11,136 clones from
NCI CGAP Sub2 (IMAGE CloneIDs 2712456-2723591) (30% of
the driver population). Subtraction was performed as
previously described (Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
                                                                                                                                                  TAG_TISSUE=lung
TAG_LIB=NCI_CGAP-Lul3
TAG_SEQ=GCCGG"
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                             10.3%;
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0;
Score 82.8; DB 7;
Pred. No. 2.9e-08;
0; Mismatches 2;
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                                                          Length 429;
      Indels
   0,
   Gaps
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626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685

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REFERENCE
AUTHORS
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                                                                                                                                                                         Query Match 10.3%;
Best Local Similarity • 97.7%;
                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on wrong Possible reversed clone: polyT not found Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 350.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
1 (bases 1 to 448)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA663771
448 bp mRNA linear EST 15-DEC ae68h10.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969379 3' similar to SW:JNK3_RAT P49187 STRESS-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA663771.1 GI:2617762
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  ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                              GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAATTC
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                                                                                                                                                    Conservative
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314 286 1810
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                                                                                                                                                                                                                                                                  /dev stage="14 years old"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene_schizo brain SII"
/clone_lib="Stratagene_schizo brain SII"
/note="Wector: Bluescript SKr; Site_1: EcoRI; Library
/note="Wector: Bluescript SKr; Site_1: EcoRI; Library
/constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excleed. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:969379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="schizophrenic brain S-11 frontal lobe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="male"
                                                                                                                                                 0,
                                                                                                                                                                      Score 82.8; DB 1;
Pred. No. 2.9e-08;
                                                                                                                                                 Mismatches
                                                                                                                                                                                              DB 1;
                                                                                                                                                                                              Length 448;
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Matches

84;

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Gaps

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354

626 GTACCTGAAGGAGGAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library preparation: Dr. M. Bento Soares, Univeristy of IowacDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of IowaDNA Sequencing by: Dr. M. Bento Soares, Univeristy of IowaClone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory for Computational University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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1 (bases 1 to 512)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two appr
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                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
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319 335 9565
                                                                                                                      /tissue_type="Retina Foveal and Macular"
/dev stage="adult"
/lab_host="pH108 (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CKI"
/clone_lib="UI-E-CKI"
/note="Organ: eye; Vector: pT7T3-Pac (pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CKI is a normalized CDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo. Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
CDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTCC. This library was created for the program,
Gene Discovery in the Visual System, supported by National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="UI-E-CK1-agb-1-15-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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                              10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _type="mRNA"
Pred. No. 2.9e
0; Mismatches
                        Score 82.8; DB 3;
Pred. No. 2.9e-08;
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                                                    Length 512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dept
MA 02
Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM508552 595 bp mRNA linear EST 12-MAI i137a11.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 M. musculus cDNA clone IMAGE:5943836 5' similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:2006708 This sequence now available from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Other_ESTs: ii37all.xl
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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EST.
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h quality sequence stop: 430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617-495-8557
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                                                           /note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five libraries representing EIO.5/12.5 pancreatic bud, EI6.5 pancreas, newborn pancreas, adult pancreas; and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies) CDN2 was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram
single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded
                                                                                                                                                                                                                                                                                                                             N1-MMS1"
                                                                                                                                                                                                                                                                                                                                                                        /lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="Both for embryonic & newborn, male for adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGE:5943836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                _stage="Embryonic day 10.5, E12.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                     host="DH10B"
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411 ATTACTTCCTTGTAGATAAGTTCTTT 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Good hit to opposite strand read. MOUSE-PANCREAS VERIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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CK825957

ik36f03.y5 HR85 islet Homo sapiens cDNA clone IMAGE:5783165 5'
similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: sim Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-Harvard Pancreas EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dmelton@biohp.harvard.edu
ad is a 5' RESEQUENCE of
/clome lib="HR85 islet"
/note="Torgan: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Xho1; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -lkb. 5'
XhoI site was destroyed after directional cloning.
Amplified once Contact information: Hitoshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
1314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                           /clone="IMAGE:5783165"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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ACCESSION
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KEYWORDS
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BQ287873
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AUTHORS
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    Query Match
Best Local Similarity
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1 (bases 1 to 618)

1 (bases 1 to 618)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Melton, D., Brown, J., Kenty, G., Gradwohl, G., Clifton, S., Lemishka, I., Scearce, M., Brestelli, J., Gardwohl, G., Clifton, S., Hiller, I., Marra, M., Pape, D., Wylle, T., Martin, J., Bilstain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine, Panoreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information

obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ287873

618 bp mRNA linear EST 14-MAY-2002 ik36f03.x1 HR85 iklet Homo sapiens cDNA clone IMAGE:5783165 3' sinilar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ287873.1 GI:20658904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iomo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 369.
Location/Qualifiers
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                                                                                   Not1; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinouesimgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                         /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5783165"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"

ol_type="mRNA"
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                                                                                                                                                                                                                                                                                    lib="HR85 islet"
    Score 82.8; DB 3; Pred. No. 3e-08;
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                      Length 618;
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Query Match
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: JENREV (CAGGAAACAGCTATGACC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: BresaGen, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HESC4_139_B07.g1_A037 NIH_MGC_262 Homo sapiens cDNA clone IMAGE;7971903 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/ CIONE LIDE NATURE CASE
/ (note "Mector: DExpress-1; Site 1: NotI; Site 2: EcoRV;
/ (note "Mector: DExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells Isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BGO1.
Possitive for Nestin and Musashi expression. Passage number
18. cDNA primed using oligo-dT primer:
5'-pGACTACTTCTACATCGCAGCGCGCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH MGC 259). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below Phred quality 16. Note:
this is a Mammalian Gene Collection library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="embryonic stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:7971903"
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|mol_type="mRNA"
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10.3%;

Score 82.8;

DB 10;

Length 921;

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REFERENCE
AUTHORS
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BI824308/c
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VERSION
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Best Local S
Matches 84
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                                                                                         989
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                                             42
                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
Plate: LLAM11453 row: a column:
High quality sequence stop: 825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.

1 (bases 1 to 933)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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BI824308
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603040725F1 NIH_MGC_115 Homo sapiens
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTC 685
                                                                     ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                           GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTTCTTGAATTC
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                                             ATTACTTCCTTGTAGATAAGTTCTTT 17
                                                                                                                                       GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTACTTCCTTGTAGATAAGTTCTTT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (human)
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                   /clone lib="NIH MGC 115"
/clone lib="NIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector: }
/note="Organ: pooled brain, lung, testis; Vector: }
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5181582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lab_host="DH10B"
                                                                                                                                                                                                                                                      10.3%;
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                                                                                                                                                                                                                           Score 82.8; DB 2;
Pred. No. 3.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA linear EST 04-OCT-2001 CDNA clone IMAGE:5181582 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inc.
                                                                                                                                                                                                                                                                           Length 933;
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                     ACCESSION
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KEYWORDS
  VERSION
                                                                                                                 RESULT 15
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JOURNAL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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                                                                                                                                                                                         380
                                                                                                                                                                                                                                  686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                           626 GTACCTGAAGGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                                                            83;
BG219861 315 bp mRNA linear
RST39628 Athersys RAGE Library Homo sapiens cDNA,
BG219861
BG219861.1 GI:13745882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RZPD; IMAG9998K0612866.

RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPDJ (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101

Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human UnigeneSet -
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (Dases 1 to 462)
Ebert,L., Heil,O., Hennig,S., Neubert,P.,
Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX282592 462 bp mRNA linear EST 04-MAR-2003 BX282592 HR85 islet Homo sapiens cDNA clone IMAGp998K0612866 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RZPD Deutsches Ressourcenzentrum
Im Neuenheimer Feld 580, D-69120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="HRB5 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: prining.
NotI; Site 2: XhOI; cDNA made by oligo-dT prining.
Size-selected on agarose gel. Average insert size-lkb. 5'
XhOI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab); Washington University
Metabolism Div. (Alan Permutt Lab); Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGp998K0612866 ; IMAGE:5783165"
/tissue_type="burified pancreatic islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                             10.2%;
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                                                                                                                                                                                                                                                                                                                                                                       Score 81.8; DB 4;
Pred. No. 4.9e-08;
0; Mismatches 3
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Heidelberg, Germany
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Seq primer:

FEATURES

COMMENT

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ORIGIN

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REFERENCE
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Best Local Similarity
Matches 81; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                              1 (bases 1 to 386)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brionøs, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                   BF858136
QV1-FT0202-131100-470-c12
BF858136
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechmol. 19 (5), 440-445 (2001)
                  Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                               Simpson, A.J.
                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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216 361 9596
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Location/Qualifiers
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/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression / Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db xref="taxon:9606"
/cell_line="HT1080"
  Acad. Sci. U.S.A.
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Pred. No. 1e-07;
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FT0202 Homo sapiens
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                                                                                                                                                               Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contart.
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi In
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 457)

Melton, D., Brown, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB069160 457 bp mRNA linear EST 21-JAN-2003 is13g01.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6364968 3' similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: puc 18 forward High quality sequence stop: 386. Location/Qualifiers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV1&t2=QV1-FT0202-
131110-470-c12&t3=2000-11-13&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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/mol_type="mRNA"
/db xref="taxon:966"
/db xref="taxon:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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Pred. No. 1e-07;
0; Mismatches
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REFERENCE
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BG194386/c
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KEYWORDS
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RST13533 Ath
BG194386
BG194386.1
EST.
                                       3201 Carnegie Ave, Cleveland, OH
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 397.
                                                                                                                                                                                                                Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random activation of gene expression

activation of gene expression

Nat. Bistechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
1 (bases 1 to 789)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                           Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=Torgan: Pancreas; Vector: pBluescript SK(-); Site 1: Not1; Site 2: XhO1; cDNA made by oligo-dT priming.

Size-selected on agarose gel. Average insert size ~1kb. 5'
XhO1 site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
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/mol_type="mRNA"
/db_xref="taxon:9606"
                    Location/Qualifiers
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/lab_host="DH10B"
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Pred. No. 1e-07;
0; Mismatches 1;
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Matches 80
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.

1 (bases 1 to 257)

1 (bases 1 to 257)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                         3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Scott J. Cain Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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RST28923 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence
BG209408
                                                                                                                                                                                                                                                                                                                                                                    Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG209408.1
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/organism="Homo sapiens"

/mol_type="mRNA"

/db xref="taxon:9606"

/cell_line="HT1080"

/clone_lib="Athersys RAGE Library"

/clone_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression',

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."
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/db xref="taxon:9606"
/db xref="taxon:9606"
/cell line="HT1080"
/clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/note="Gee 'Creation of Genome-wide Protein Expression',
Inbraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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Pred. No. 1.1e-07;
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h 9.8%; Similarity 97.6%; 80; Conservative

Score 78.8; DB 2; Pred. No. 2.3e-07; 0; Mismatches 2;

2.3e-07; ches 2;

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CJ443965 GI:77250642
EST.
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National Institute of Biomedical Innovation
Saito-Asagi 7:6-8, Ibaraki, Osaka, 567-0085,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirata, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K. Macaca fascicuraris cDNA database Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 81-72-641-9811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Naoki Osada
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                                                                                                                                        GCACCTGAAGGAGAAGGCTGTCCTTTTACTACGCCATTTTTAGTCTTCTTCTTCTGAGTTC
                                                                                                                                                               GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC
                                                           ATTACTTCCTTGTAGATAAGTTCTTT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCCTTGTAGATAAGTTCTTT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .l: nosada@nibio.go.jp
http://genebank.nibio.go.jp/gbank/.
Location/Qualifiers
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                           /clone_lib="macaque brain cDNA library OccE"
/note="Vector: pME18S-FL3 (Acc.No. AB009864); Site_1:
DrailI (CACTGTGTG); Site_2: DrailI (CACCATGTG); lst strand
cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
synthesized using specific 5' and 3' primers and amplified
by PCR. The PCR product was digested with Stil and size
selection was performed to exclude fragments <1.5kb.The
Sfil-digested PCR product was cloned into distinct DrailI
sites of pME18S-FL3. XhoI sites just outside the DrailI
sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="cerebellum cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'eex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Macaca fascicularis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="QccE-21545"
                                                                                                                                                                                                                                     9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                Score 78; DB 5; Le
Pred. No. 3.9e-07;
0; Mismatches 5;
                                                                                                                                                                                                                                                        Length 836;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Japan
                                                                                                                                                                                                                  <u>,,</u>
                                                                                                                                        63
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RESULT 22
CF408692/c
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RESULT 21

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REFERENCE
AUTHORS
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TITLE
JOURNAL
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                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuherberg, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZ0459H0638) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459H0638
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
1715 CTTCCTTGTAGATAAGTTCTTT 1694
                                            690
                                                                                                                                      630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTT
                                                                                                                                                                                  79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pongo pygmaeus mRNA; cDNA DKFZp459H0638 CR859197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I (bases 1 to 2693)
Koehrer, K., Beyer, A., Mewes, H.W., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pongo pygmaeus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Pongo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus (orangutan)
                                    CTTCCTTGTAGATAAGTTCTGT 711
                                                                                          CTGAAGGAGAGGCTGTCCTTTTACTACGCCATTTTTI
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                VRHKILFPGRDYIDQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFP
DSLFPADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPP
PQIYDEQLDEREHTIDEWKELIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ"
                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MSKSKVDNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAY
DAVLDRNVALKKLSRPFQHQTHAKRAYRELVLMKCVNHKNIISLLNVFFTQKTLEGFQ
KDVYLVMELMBAULGQVIQMELDHERMSYLLYQMLCGIKHLHGAGIIHRBUFTAKFBNIVYK
SDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMGYKENVDIMSVGCIMGEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="cortex"
/clone_lib="459 (synonym: pcor1). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="hypothetical protein"
/protein_id="CAH91384.1"
/db_xref="GI:55729297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DKFZp459H0638"
638. .1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="mitogen-activated protein kinase
sapiens), differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="DKFZp459H0638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp459H0638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:55729296
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                                                                                                                                                                                                        9.7%;
                                                                                                                                                                                  0
                                                                                                                                                                                                      Score 77.2; DB 6; Pred. No. 6.5e-07;
                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                              Length 2693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 isoform 3 (Homo
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                                                                                          1716
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JOURNAL COMMENT
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ORGANISM
                                                                                                                                                                                   CJ491725/c
LOCUS
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                                                      SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                         EYWORDS
                                                                                                              VERSION
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Best Local S
Matches 80
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                                                                                                                                                                                                                                                                       420
                                                                                      CJ491725 MACAQUE testis cDNA library QtsA Macaca fascicularis cDNA clone QtsA-19671 5', mRNA sequence.

CJ491725 CJ491725 GI:77292599

EST.
                                                                                                                                                                                                                                                                                                                                                                                                                  80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville,
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Ensert Length: 1678 Std Error: 0.00
Seq primer: T7: TAATACGACTATAGGG
High quality sequence start: 37
High quality sequence stop: 762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yi,Y., Desai,R., Olarte,M.
Expressed sequence tags fr
Unpublished (2003)
Other_ESTs: CH3#056_B08T3
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                      Macaca fascicularis
                                                                     Macaca fascicularis (crab-eating macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: George AL
Division of Genetic Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canida
Canis.
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946 bp mRNA linear EST 02-SEP-20
CH3#056_B08T7 Canine heart normalized CDNA Library in pBluescript
Canis familiaris cDNA clone CH3#056_B08 5', mRNA sequence.
CF408692
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EST.
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                                                                                                                                                                                                                                                                                          ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                             GCACCTGAAGGAGAAGGTTGTCCTTTTACAACACCGTTTTTAGTCTTTTCTTCCGAATTC
                                                                                                                                                                                                                                                                       ATTACTTCCTTGTAGATAAGTTCTTT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 946)
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector Not1; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day feaal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    day feta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9615"
/clone="CH3#056_B08"
/tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="Canine heart normalized cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="heart"
dev_stage="mixed developmental stages (adult, 30 day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Canis familiaris"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               93.0%;
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ce tags from Canine heart
                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                Score 76.4; DB 5;
Pred. No. 9.1e-07;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ა.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                              421
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AUTHORS
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DA807178/c
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VERSION
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AUTHORS
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JOURNAL
                                     TITLE
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                                                                                                                                                                                                                                                                                                       sequence.
DA807178
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                                                                                                                                                                                                                                                                                                                                             DA807178
DA807178 OCBBF3
                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                          DA807178.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Unpublished (2005)
Contact: Nacki Osada
Division of Biomedical Resources
National Institute of Biomedical Innovation
Saito-Asagi 7-6-8, Ibaraki, Osaka, 567-0085,
Tel: 81-72-641-9016
Fax: 81-72-641-9016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nosada@nibio.go.jp
URL: http://genebank.nibio.go.jp/gbank/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osada, N., Hida, M., Kusuda, J., Tanuma, R., Suzuki, Y., Sugano, S. and Hashimoto, K. Macaca fascicuraris cDNA database
                                                                                                                                             /Clone lib="macaque testis cDNA library QtsA"
/note="Vector: pME185-FL3 (Acc.No. AB09864); Site 1:
Draili (CACTGTGTG); Site 2: Draili (ABCOS866); lst strand
cDNA was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
synthesized using specific 5' and 3' primers and amplified
by PCR. The PCR product was digested with Sfil and size
selection was performed to exclude fragments <1.5kb.The
Sfil-digested PCR product was cloned into distinct Draili
sites of pME185-FL3. XhoI sites just outside the Draili
sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="testis"
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Score 75.6; D
Pred. No. 1.4e
0; Mismatches
                             ; DB 5;
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Gaps

Hominidae, Homo.

1 (bases 1 to 568)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Kimura, K., Wakamatsu, A., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, J., Sekine, M., Tsono, Y., Irie, R., Kushida, N., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yokoi, T., Kondo, H., Wagatsuma, M., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens cDNA mRNA linear E EST 11-NOV-2005 4 5', mRNA Wagatsuma, M.,

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JOURNAL
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COMMENT
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AUTHORS
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BF857793
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                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 408)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rudwig Institute for Cancer No. 4 and
                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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BF857793
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NEDO human cDNA project (New Energy and Industrial Technology

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one

pass sequencing: RAB.
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2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
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16344560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTCATTACTTCC 509
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                                                                      +55-11-2704922
+55-11-2707001
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/db_xref="taxon:9606"
/clone="OCBBF3022734"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
/dev_stage="fetal"
/clone_lib="OCBBF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Vector: pME18SFL3"
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Pred. No. 1.5e-06;
D; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 bp mRNA linear
FT0202 Homo sapiens cDNA,
                                                                                                                                                                                                                                                        97 (7), 3491-3496 (2000)
                                                                                                                                        4 andar, 01509-010,
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AW314598/c
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases cai
v0.980904.e. Vector identified by
and _minmatch 12 options.
                                                                                                                                                                                                                                                                                 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Seq primer: put lB forward
High quality sequence stop: 325.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 9 row: D column: 1
                                                                                                                                           PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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Similarity 90.7%;
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                                                                                   te: 9 row: D column: 1
primer: ATTTAGGTGACACTATAG
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/mol_type="mRNA"
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/dev_stage="Adult"
/clone_lib="FT0202"
/note="Organ: prostate_tumor; Vector: pucl8; Site_1: SmaI;
/site_2: SmaI, A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
/mol_type="mRNA"
                                                                 Location/Qualifiers
                        organism="Bos taurus"
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Pred. No. 4.6e-06;
0; Mismatches 8
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                                                                                                                                                                                                                    cross_match
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 686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with
trimmed with the aid of the trim_alt optio
cross_match v0.990329.
Plate: RLK8072 row: G column: 21
Seq primer: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, T.P.L., Roberts, A. Wray, J.E. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Boyidae; Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DN543033.1 GI:61001631
EST.
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DN543033
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (cattle)
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                                                 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAATTC
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                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARS, US Meat Animal Research Center
x 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                           /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embros."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 20 and day 40 embrvos."
                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC_7BOV"
                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9913"
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/lab_host="DH10B"
/clone_lib="MARC 4BOV
                                                                                                                                                                                                                                                                                                                 organism="Bos taurus"
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                                                                                                           88.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts, A.J., Echternkamp, S.E.,
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                                                                                                           Score 70; DB 9;
Pred. No. 2.6e-05;
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Pred. No. 2
                                                                                              Mismatches
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cdna
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2.5e-05;
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on. Vector identified with
                                                                                              Indels
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ACCESSION
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AUTHORS
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KEYWORDS
SOURCE
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BE752856/c
                                                                        RESULT 29
BE752838/c
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  VERSION
                                                        Focus
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PUBMED
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Best Local S
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                                                                                                                                                                                      686 ATTACTTCCTTGTAGATAAGTTCT 709
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., & Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 bp mRNA linear
205445 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE752856
BE752856.1 GI:10166848
551
205425 MARC 2BOV Bos taurus
BE752838 .1 GI:10166830
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Plate: 46 row: P column: 10
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 402 762 4366
Fax: 402 762 4390
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                               /db xrel="cav..../
/tissue_type="pooled"
/tissue_type="pooled"
/lab host="H108"
/clone_lib="MARC_2BOV"
/clone_lib="WARC_2BOV"
/note="Vector: pCMV_SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary_made_from_pooled_tissue_from_testis, thymus,
semitendonosus_muscle, longissimus_muscle, pancreas,
...^ andometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9913"
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Pred. No. 3.1e-05;
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                                      mRNA linear
', mRNA sequence
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REFERENCE
AUTHORS
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DV915617/c
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DV915617
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Bos taurus
Bos taurus
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1 (bases 1 to 916)
Moore, S., Alexander, L., Browns
Tanaguchi, M., Wang, Z., Yu, J.,
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                               DV915617.1
EST.
                                                                                                                                                                        Bos taurus
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PO Bo
Tel:
                                                                                                                                                                                                  Bos taurus (cattle)
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Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACTTCCTTGTAGATAAGTTCT 709
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Box 166, Clay Center, NE
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402 762 4390
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/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: 9a
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
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/mol_type="mRNA"
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                                                    to 916)
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  Brownstein, M., Gi
Yu, J., Prange, C.,
                                                                                                                                                                                                                                                                                                                                          Bos taurus
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NE 68933-0166, UK
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                                                                                                                                                                                                                                                                                                                                       cDNA clone
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  Guan, L., Lobo, S., Meng, Y., Schreiber, K., Shenmen, C.
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                                                                                                                                                                                                                                                                                                                                       IMAGE:8222610, mRNA
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SOURCE
ORGANISM
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DV915213/c
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                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 801)

1 (bases 1 to 801)

1 (Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Moore, S., Alexander, Yu, J., Prange, C., Schreiber, K., Shenmen, C., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaiff, R., Wagner, L., Del Rio, L., Gibson, S., Hanson, R., Kirkpatrick, R., Liu, J., Matsuo, C., Mayon, Santos, R.R., Stott, J., Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A. Bovine Genome Sequencing Program: Full-length cDNA Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
BC Cancer Agency
Suite 100, 570 West 7th Avenue,
Canada, V5Z 4S6
                                                                       Unpublished (2005)
Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LB0287.CR_A06 GC_BGC-28 Bos taurus cDNA clone IMAGE:8222096, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pv915213
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Contact: Robert Kirkpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: robertk@bcgsc.ca
Insert Length: 916 Std Error:
Plate: LB0288 row: F column: 1
High quality sequence stop: 916.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 1-604-707-5900 x5406 Fax: 1-604-876-3561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 100,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canada's Michael Smith Genome Sciences Centre
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/lab_host="E. coli DH10B T1 Phage resistant"
/clone_lib="GC_BGC-28"
/note="Organ: Cerebral cortex; Vector: pExpress 1; Site_1:
/note="Organ: Cerebral cortex; NotI (3' end of cDNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9913"
/clone="IMAGE:8222610"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="L1 Hereford"
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87.2%;
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                              Vancouver,
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RESULT 32
BY126616/c
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KEYWORDS
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Nikasido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikasido, I., Osato, N., Salto, R., Suzuki, H., Yamanaka, I., Nikaido, I., Osato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hassgawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Peeole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Vang, L., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Garninci, P., Yang, L., Yuan, Z., Zavolan, M., Shiraki, T., Waki, K., Kawal, J., Alzawa, K., Arabawa, T., Khiraki, T., Waki, K., Kawal, J., Alzawa, K., Arabawa, T., Kanai, K., Kawal, J., Alzawa, K., Arabawa, T., Third, K., Kawal, J., Alzawa, K., Arabawa, T., Takenak, K., Arabawa, T., Takenak, K., Arabawa, T.,
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332 bp mRNA linear EST 08-DEC-2002
BY126616 RIKEN full-length enriched, adult male brain Mus musculus
cDNA clone L630049C19 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY126616.1 GI:26237717
EST.
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Plate: LB0287 row: A column: 6
High quality sequence stop: 801.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 1-604-707-5900 x5406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTATTCACGGAGAGTGAGTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTA 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 332)
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/clone_lib="GC_BGC-28"
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/note="Organ: Cerebral cortex; Vector: pexpress 1; Site_1:
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|mol_type="mRNA"
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'clone="IMAGE:8222096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain="L1 Hereford"
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Pred. No. 5e-05;
0; Mismatches 22;
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Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Ohno,M., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Ohno,M., Sato,M., Sasaki,D., Sato,K., Shibata,K., Sato,M., Sat
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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urther details.
                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length
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/lab_host="DH108"
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/clone="L630049C19"
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Query Match
Best Local Similarity
Matches 75; Conserv

Conservative

8.6%;

Score 68.4; DB 4; Pred. No. 5.8e-05; Mismatches

DB 4;

Length 332;

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686 ATTACTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 427-537, >(CA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE652295 543 bp mRNA linear EST (
UI-M-AHO-acy-e-12-0-UI.rl NIH BMAP_MCE Mus musculus cDNA
UI-M-AHO-acy-e-12-0-UI 5', mRNA sequence.
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Mus musculus (house mouse)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/dev gtagge="27-32 days"
/dev gtagge="27-32 days"
/lab_host="PHH10B (Life Technologies)"
/clone_lib="NH10B (Life Technologies)"
/clone_lib="NH10B MAP_MCE"
/note="Vector: pT773D-PacI; Site_1: Not I; Site_2: Eco RI;
/note="Vector: pt773D-PacI; Site_2: Eco RI;
/note="Vector: pt773D-PacI; Site_2: Eco RI;
/note="Vector: pt773D-PacI; Site_2: Eco RI;
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Zivic-Miller Laboratories.
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/strain="C57BL/6J"
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McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M., Ritter, B., Tsagareishvili, R., Ronko, I., Maguire, L., Kennedy, S., Bennett, J., Waterston, R. and Wilson, R.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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53 bp mRNA linear EST 21-APR-200 mai49d11.yl McCarrey Eddy round spermatid Mus musculus cDNA clone IMAGE:6449444 5' similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: McCarrey/Eddy NIEHS Mouse
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                                                                                                                               /tissue_type="round spermatids, pooled from multiple mice"
/dev stage="60 day"
/lab_host="PH10B (phage-resistant)"
/clone_lib="McCarrey Eddy round spermatid"
/clone_lib="McCarrey Eddy round spermatid"
/note="Organ: testis; Vector: pBluescript SK+
/note="Grant testis; Vector: pBluescript SK+
(Stratagene); Site_l: XhoII; Site_2: EcoRI; cDNA oligo
dT-primed [5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTT-3'] and
directionally cloned using 5' linkers 5'-AATTCGCACAGAG-3'
and 5'-CTCGTGCGG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UniZAP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 98.3 recombinants.

References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63423."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="CD-1"
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                             8.6%;
Score 68.4; DB Pred. No. 6e-05; O; Mismatches
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RESULT 36
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AK042368
2343 bp mRNA linear HTC 02-5
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length 6
library, clone:A630085G12 product:mitogen activated protein
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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CB234404.1 GI:28285982
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDCM06 row: f column: 20
High quality sequence stop: 597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: T. Rajendra Kumar and Martin
cDNA Library Preparation: CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                     GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                         ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGE:30247531"
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                                                                                                                                                                                                           Score 68.4; DB 4;
Pred. No. 6.2e-05;
0; Mismatches 11;
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The Transcriptional Landscape of the Mammalian Genome

AL Science 309, 1559-1563 (2005)

CB (bases 1 to 2343)

RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Murata, M.,
Nashi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takku, Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A.,
Nasani, A., Maramateu, M., and Hayashizaki, Y.
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Direct Submission
Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institu
Physical and Chemical Research (RIKEN), Laboratory for Gen
Exploration Research Group, RIKEN Genomic Sciences Center
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium, Riken Genome Exploration Research Genome Science Group (Genome Network Project Core Group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN Genome Exploration Research Group, Genome Science (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)
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Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
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Functional annotation of a full-length mouse cDNA collection
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(E-mail:genome-res@gsc

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                                                                                                                                                                             protein kinase 10, full AK036275
AK036275.1 GI:26085131
HTC; CAP trapper
Mus musculus (house mouse musculus
                                                                                                                                                                                                                                                                                                                                     2729 bp mRNA linear Mus musculus 16 days neonate cerebellum cDNA, RIKEN enriched library, clone:9630051C24 product:mitogen protein kinase 10, full insert semanno AKO3627K
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
   Carninci, P. and Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Please visit our web site for further details.
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/db_xref="GI:26335079"
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/cd_xref="MILHFLYYCSEPTLDVKIAFCQGFDKHVDVSSIAKHYNNSKSKV
/cr_nallation="MILHFLYYCSEPTLDVKILAFCQGFDKHLDRINJAIKKISRPFQNQ
DNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAXYDAVLDRINJAILCQVIQME
LDHERKSYLLYQMCGGIKHLKBAGIIHRDLKPSNITVKSDCTLKILDFGLARTAGTSF
MMTPYTAPACHICAMGYKENVDIMSVGCIMGBWYRHKIIFPBGDYIDMNKVI
EQLGTPCPEFRYKKLQPTVIAMGYENVDIMSVGCIMGBWYRHKIIFPBGDSEHRKIXASQARD
LDSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVNNSEEKTKNGVVKGQPSPSGAAVNSSESLPPSSSVNDISSMSTDQTLASDTD
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132. .1526
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
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'db_xref="taxon:10090"
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/strain="C57BL/6J"
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                                                                                                                                                               Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, VRL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

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Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genome Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Shibata, K., Shinagawa, A., Takahashi, F., Takaku-Akahira, Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1563 (2005)
8 (bases 1 to 2729)
Adachi.J *:--729)
URL:http://genome.gsc.riken.jp/
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium, the RIKEN Genome Exploration Research Group
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Roddman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75;
                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR1&t2=MR1-FN0210-
301000-001-b10&t3=2000-10-30&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF854904.1 GI:12242648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF854904 561 bp mRNA linear MR1-FN0210-301000-001-b10 FN0210 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCACCTGAAGGCGAGGGCTGGCCTTTGACTACGCCATTCTTAGTCTTCTCTTCTGAGTTC 1715
                                                                                                                                                                                                                                                                                +55-11-270700:
                                                                                                            quality sequence stop: 559.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            match=2139)
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="cerebellum"
/clone Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days neonate"
1. .2729
                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="mitogen activated protein kinase 10 (MGD MGI:1346863 GB NM_009158, evidence: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="FANTOM_DB:9630051C24"
db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="9630051C24"
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Pred. No. 6.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                             andar, 01509-010, Sao Paulo-SP
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JOURNAL PUBMED REFERENCE AUTHORS

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yeamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburnar, M., Batalov, S., Casavant, T., Fleischmann, W., Gasaterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Chiwa, H., Ouackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,

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SOURCE
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AK163206/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
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Best Local
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus 7 days neonate cerebellum cDNA, RIKEN enriched library, clone:A730093C22 product:mitogen protein kinase 10, full insert sequence.
AK163206
AK163206.1 GI:74190275
                                                                                                                                                                                                                                                                                                                            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTC; CAP trapper.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                        11042159
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/clone_lib="RN0210"
/note="Organ: prostate_normal; Vector: puc18; Site_l:
/note="Organ: prostate_normal; Vector: puc18; Site_l:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.8%;
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Pred. No. 8.3e-05,
0; Mismatches
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Fletcher, G., Pajte, M., Gartholdi, M., Gustincin, S., Hill, D., Hoffmann, M., Tume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Marchlomi, L., Manhima, J., Mazzarelli, J., Kombaerts, P., Nordone, P., Marchlomi, L., Manhima, J., Mazzarelli, J., Kombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, J., Sakmotco, N., Sasaki, H., Wanter, A., Saraki, M., Wanter, C., Wannick, P., Shizhel, S., Saraki, H., Wanter, C., Wannick, P., Shizhel, S., Saraki, H., Kondon, S., Khukashi, Y., Yoshida, K., Hangshar, Y., Scorch, K. P., Shizhel, S., Saraki, H., Wannick, J., Wannick, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegmer,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yaqi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Koyama,J., Koyima,M., Kato,T., Koyam,J., Koyima,M., Kato,T., Koyam,J., N., Kawashima,T., Kojima,M., Koyono,H., Nakano,K., Nicomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Panarom Componerium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genome Exploration Research Group
Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16141073
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                           /proteIn_id="BAE37234.1"
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/cb_xref="G1:74190276"
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translation="MSLHFLYYCSEPTLDVKIAFCQGFDKHVDVSSIAKHYNMSKSKV/
DNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLLRNVAIKKLSRFFQNQ
DNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLLRNVAIKKLSRFFQNQ
DNQFYSVEVGDANLCQVIQME
                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product; mitogen activated protein
kinase 10 (MGD MGI:1346863 GB|BC046625, evidence: BLASTN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6J"
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LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="7 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="cerebellum"/clone_lib="RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FANTOM_DB:A730093C22"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                             codon_start=1
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RESULT 41
CF535846/c
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CB607972/c
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AMGNNUC:NRDG1-00127-G9-A nrdg1 (10855) Rattus
CB607972
CB607972.1 GI:29547657
CF535846 570 bp mRNA
UI-M-GHO-cha-a-06-0-UI.rl NIH BWAP GHO Mus
IMAGE:30533669 5', mRNA sequence.
CF535846 CF535846.1 GI:34587814
                                                                                                                                                                                                                                                 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              One Amgen Center Drive, Thousand Oaks, Tel: 805 447-4881
Plate: 00127 row: g column: 9.
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Amgen Rat EST Program
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                               ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                        GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC
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                                                                                                                                ATTACTTCCTTGTAGATGAGTTCTTT 353
                                                                                                                                                                                        GCACCTGAAGGTGAGGGCTTGGCCTTTGACTACGCCGTTCTTAGTCTTCTTCTTGAGTTC
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                                                                                                                                                                                                                                                                                                              /clone="nrdg1-00127-g9"
/tissue_type="Dorsal Root Ganglia"
/clone_Tib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; ratdorsal root ganglia"
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LIYKEVMNSEEKTKNGVVKGQPSPSA"
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EQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARD
                                                                                                                                                                                                                                                                                                                                                                                                                                               127 row: g column:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Rattus norvegicus"
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Pred. No. 0.00014;
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BM944347/c
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BM944347 BM944347.1 EST

GI:19427932

Mus musculus (house mouse)

BM944347
UI-M-EHOp-bvq-f-13-0-UI.r1 NIH\_E
IMAGE:5695500 5', mRNA sequence

BMAP\_EHOP

mRNA

linear EX

EST 14-MAR-2002

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KEYWORDS
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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Mus musculus

Mus musculus

Chorde
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following repetitive elements were found in this cDNA sequence: 383-493, >(CA)n#Simple_repeat
Seq primer: pYX-5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                    Similarity
                                                       CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                         CTGAAGGCGAGGGCTTGGCCTTTGACTACGCCATTCTTAGTCTTCTCTTCTGAGTTCATTA
CCTCCTTGTAGATAAGTTCTTT 102
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                     /dev stage="1, 5, and 15 days newborn"
//lab host="DH108 (T1 phage resistant)"
//clome 11b="NIH BMAP GH0"
//clome 11b="NIH BMAP GH0"
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
grimer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                    8.2%;
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                                                                                                                                                                                                                                                    Score 66;
Pred. No.
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0.00021;
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                                                                                                                                                                                                                                                                                                                                                                                                           690
                                                                                                                                                                                                                                                                                                                                                                                                                                                               335
                                                                           CX221469 639 bp mRN
MNS38129 Mouse Neurosphere Normalized
cDNA 5', mRNA sequence.
CX221469 CX221469 CX221469.1 GI:56876761
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammaila; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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/dev stage="whole brain"
/lab_host="DH10B (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAp EHOp"
/clone lib="NIH BMAp EHOp"
/clone lib="NIH BMAp EHOp"
/site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6"
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Pred. No. 0.00
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library
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                               Euteleostomi;
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RESULT 44
CF951683/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337
                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72;
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 721)
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF951683
UI-M-HL0-cnc-a-15-0-UI.rl NIH_BMAP_HL0 Mus musculus
IMAGE:30633902 5', mRNA sequence.
The following repetitive elements were sequence: 409-519, >(CA)n#Simple_repeat
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EST.
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1 (bases 1 to 639)
Williams,C., Wirta,V., Lundeberg,J. and Frisen,J.
Expressed sequence tags of cDNA clones from murine
Unpublished (2005)
Contact: Williams, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +46855378481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +46855378332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cecilia.williams@biotech.kth.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlbaNova University Center,
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/note="Organ: Adult brain; Vector: pcMVSport6.0; A cDN.
library was constructed in pcMVsport6.0 from RNA isola.
from neurospheres of adult male and female mice. Custon
normalized cDNA library by Invitrogen/ResGen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
/mol_type="mRNA"
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Seq primer: pYX-5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi, Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 740)
NIH-MGC hetp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM943588 740 bp mRNA linear EST 14-MAR-2002 UI-M-EM0-bvm-m-16-0-UI.rl NIH_BMAP_EM0 Mus musculus cDNA clone IMAGB:5694135 5', mRNA sequence.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999
                                              sequence: 498-608, >(CA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                          The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCTTGTAGATAAGTTCTTT 128
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                      primer: pYX-5
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                                                                                                                              clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH)."
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/dev stage="9.5 dpc"
/lab_host="9H10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HL0"
/clone_lib="NIH_BMAP_HL0"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
/site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
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Pred. No. 0.00022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 CTGAAGGCGAGGGCTTGGCTTTGACTACGCCATTCTTAGTCTTCTCTCTGAGTTCATTA
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                                                                                                                                                                                                                                                                                  Unpublished (2004)

On Feb 2, 2005 this sequence version replaced gi:58509682.

Other_ESTs: JGI CAAL8222.fwd

Contact: Lindquist,E.A., Richardson,P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel, Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipi Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 802)
Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C. Brokstein, P. and Lindquist, E.A.

DDE Joint Genome Institute Xenopus tropicalis EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CX852086 802 bp mRNA linear EST 03-AUG-
JGI_CAAL8222.rev NIH_XGC_tropBrn4 Xenopus tropicalis cDNA clone
IMAGE:7666337 3', mRNA sequence.
                                                                             Email: cdna@jgi-psf.org
Tissus Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
                                                                                                                                                                                                                                Tel: 925 296 5600
Fax: 925 296 5710
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/(lab host="bild" (Tiphage resistant)"
/(clone libb"NIH BMAP EMO"
/(clone libb"NIH BMAP EMO"
/(note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/(note="Organ: brain; Vector: pYX-Asc; Site_1: For I;
/(note="Organ: brain; Vector: pXY-Asc; Site_1: Roc I;
/(site_1: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIWH), Hemin Chin, Ph.D., program coordinator."
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/lab_host="DH10B (T1 phage ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="whole brain"
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                                                                                                                                                                                                                                                                                                                                                                                                       clone RBC20650 5', mRNA
BP485311
BP485311.1 GI:85969903
EST.
                                                                                                                                                         Laboratory of Molecular Genetics Institute for Molecular and Cellular Regulation, Shows-machi 3-39-15, Maebashi, Gunma, 371-8512, JTel: 81-27-220-8832
                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP485311
BP485311 Rattus
                                                                                                                                                                                                                                            Takeda, J., Wang, H. and Horikawa, Y. Expression profile of mRNAs from rat Unpublished (2006)
                                                                                                                                                                                                                              Contact: Yukio Horikawa
                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
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Plate: CAAL 0085 row: 1 column: 15
                                                                                                                        Email: yhorikaw@showa.gunma-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 794
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                    /db_xref="taxon:10116"
/clone="RBC20650"
                                                   organism="Rattus norvegicus"

mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7666337"
                                                                                                      ocation/Qualifiers
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Pred. No. 0.00022
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BU389929/c
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KEYWORDS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PO Box 88, Manchester, M60 1QD, Tel: 01612008930
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
A Comprehensive Collection of Chicken cDNAs
Corr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Simon. Hubbard@umist.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simon Hubbard Department of Biomolecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                            /dev stage="16 day embryo"

/lab host="DH10B"
/clone lib="CSEQCHN57"
/clone lib="CSEQCHN57"
/clone lib="CSEQCHN57"
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/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
/note="Organ: brain; Vector: pBluescript was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="ChEST780f8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Score 64; DB 3; Le
Pred. No. 0.00059;
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Pred. No. 0.0005;
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Query Match
Best Local Similarity
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1283656 NCCCWA O3RT Oncorhynchus mykiss cDNA 3', mRNA sequence
CX143962 CX143962.1 GI:57000617
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 645)
                                                             Oncorhynchus mykiss (rainbow Oncorhynchus mykiss
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Oryzias latipes
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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BJ725204 MF01FFA cDNA Oryzias
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Medaka EST Project in Takeda's lab
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/sex="mixture of female and
/tissue_type="whole embryo"
/dev_stage="fry stage 40"
/clone_lib="MF01FFA cDNA"
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/strain="Hd-rR"
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Seq primer: GTAATACGACTCACTATAGGG
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Plate: 116 row: J cc
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Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
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Contact: Rexroad CE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 304 724 8340 x2129
Fax: 304 725 0351
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/mol type="mRNA"
/db_xref="texcon:8022"
/tissue_type="pooled"
/lab_host="DH10B"
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

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15,
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APPLICANT: MCKAY, Robert A.

APPLICANT: Monia, Brett

APPLICANT: Monia, Brett

APPLICANT: Mero, Pam

FITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

FILE REFERENCE: ISPH-0318

CURRENT APPLICATION NUMBER: US/09/130,616C

CURRENT APPLICATION NUMBER: US/09/130,616C

CURRENT APPLICATION NUMBER: 08/910,629

EARLIER APPLICATION NUMBER: 08/910,629

EARLIER APPLICATION NUMBER: 08/910,629

EARLIER FILING DATE: 1997-08-03

NUMBER OF SEQ ID NOS: 178

SEQ ID NO 178

LENGTH: 1505

ORGANISM: Homo Bapien

US-09-130-616-178
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                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 178, Application US/09130616C Patent No. 6221850
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pa
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
APPLICANT: Desanlis-Cremond, Francine
TITLE OF INVENTION: Polypeptides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650B
CURRENT FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aventis Pharmaceuticals Inc.
APPLICANT: Fournier, Alain
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTACTTCCTTGTAGATAAGTTCTTT 1198
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US-09-949-016-13749
US-09-949-016-68481
US-09-949-016-13753
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Pred. No. 4e-11;
0; Mismatches 2;
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Sequence
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13749, A
68481, A
13753, A
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; LIBRARY: GENBANK
; CLONE: 91463124
US-09-023-655-952
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
                                                                                                                                Matches
                                                                                                                                                                Query Match
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Patent No. 66
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Best Local Similarity 97.7%;
                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORIEY AGENT INFORMATION:
ATORIEY Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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TOPOLOGY: li
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CITY: PALO ALTO
STATE: CALIFORN
                                                                                                                              Local Similarity 97.
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                                                                                                                                                                                                                                                                                                                               LENGTH: 1505 base pairs
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ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                     GTACCTGAAGGAGAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                         GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                           linear
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                                                                                                                            Score 82.8; DB 3;
Pred. No. 4.1e-11;
0; Mismatches 2
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Pred. No. 4.1e-11;
0; Mismatches 2
                                                                                                                                                                    DB 3;
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                                                                                                                                                                Length 1505;
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                                                           1264
                                                                                             685
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RESULT 5
US-09-165-522-3/c
US-09-165-522-3/c
; Sequence 3, Application US/09165522
; Patent No. 6943000
; GENERAL INFORMATION:
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US-09-165-522-1/c
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Best Local S
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Patent No. 6943000
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence LOCATION: 68...1459
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOPTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-OCt-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                         1323 GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                686
                                                                                                                                                                                                                                                                                                                                                                        1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                             ATTACTTCCTTGTAGATAAGTTCTGT 711
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STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1505 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative .
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Rakic, Pasko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%;
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l, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82.8; DB 3;
Pred. No. 4.1e-11;
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US-09-566-921-34/c
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            SOFTWARE: PER
SEQ ID NO 34
LENGTH: 2677
                                                                                                                                                                            Patent No. 6682888

GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Carla M.
APPLICANT: Edwards, Carla M.
APPLICANT: Edwards, Carla M.
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09566921 Patent No. 6682888
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                                                                                              FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: LBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1419 ATTACTTCCTTGTAGATAAGTTCTTT 1394
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Davis, Roger J. Flavell, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                 PERL Program
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STATE: MA
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Yang, Di
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Whitmarsh, Alan
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DB 3;

Length 2367;

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Gaps

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US-09-130-616-177/c
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APPLICANT: Desanlis-Cremond, Francine
APPLICANT: Desanlis-Cremond, Francine
TITLE OF INVENTION: Polypeptides Derived From JNI
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650B
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
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Sequence 177, Application US/09130616C Patent No. 6221850
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aventis Pharmaceuticals Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO. 6682888 413797.5
NAME/KEY: unsure
LOCATION: 2024
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1306
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nes 84; Conserv
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Maury, Isabelle
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Pred. No. 4.8e
0; Mismatches
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4.8e-11;
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; SEQ ID NO 177
; LENGTH: 1773
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Patent No. 6943000
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,9
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,522

APPLICATION OF THE PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/660,995

FILING DATE: 03-0CT-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: JNK3 MODULATORS AND NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1343 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCTTGTAGATAAGTTCTTT 1262
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
                                                                                                                    TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 225 Franklin Street
                                      ENGTH: 1773 base pairs
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ADDRESSEE: Fish & Richardson P.C.
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Flavell, Richard
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                                                                                                                                                                                              32,983
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                                                                                                                                                                              10363/005001
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RESULT 11
US-09-130-616-174/c
; Sequence 174, Application US/09130616C
; Patent No. 6221850
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; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c',
US-09-771-161A-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
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                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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LENGTH: 2131
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Best Local Similarity
                                                     APPLICANT: MCKAY, Robert A. APPLICANT: Dean, Nicholas M. APPLICANT: Monia, Brett APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
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atent No. 6936450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Local Similarity 98.8%;
hes 81; Conservative
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA FEATURE:
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ilarity 98.8%;
Conservative
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Pred. No. 1.7e
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Pred. No. 1.8e-10;
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1.7e-10;
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US-09-016-434-1389
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                                                                                                                TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 131
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Janice
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CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 178
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                              TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                              LIBRARY:
                                                                                    STRANDEDNESS:
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CALIFORNIA
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Jeffrey J. Seilhamer
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Pred. No. 1.8e-10;
0; Mismatches 1
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US-09-165-522-6/c
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 1036:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
TELEFAX: 617/542-5076
TELEFAX: 617/542-5066
TELEFAX: 617/542-5066
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                  Matches
                                                                                                                                                                   Query Match
Best Local
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Best Local
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FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/ACENT INFORMATION:
 1415
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SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskecte
COMPUTER: IBM Compatible
                                                                       1475 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1416
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ADDRESSEE: Fish & Richardson P.C.
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Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
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                                                                                                            630 CTGAAGGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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Similarity 98.8%;
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Similarity 98.8%;
CTTCCTTGTAGATAAGTTCTTT 1394
                       CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                0; Mismatches
                                                                                                                                                                 Score 80.4; DB 3; Length 2372; Pred. No. 1.8e-10;
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, NAME/KEY: Coding Sequence
; LOCATION: 224...1489
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-165-522-7
RESULT 15
US-09-566-921-33/c
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US-09-165-522-7/c
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09165522 Patent No. 6943000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Passe, J. Peter
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
                                                                         1415
                                                                                                                                              1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAN: 617/542-8906
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTMARKE: FRASTSO for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF MUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
                                                                                                          690
                                                                                                                                                                 630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTTCTGAAATTCATTA 689
                                                                                         CTTCCTTGTAGATAAGTTCTGT 711
                                                                         CTTCCTTGTAGATAAGTTCTTT 1394
                                                                                                                                              CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTGAATTCAT
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STRANDEDNESS: double
TOPOLOGY: linear
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.l, Richard
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Pred. No. 1.8e-10;
0; Mismatches 1
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                                                                                                                                                                                                                                                   Length 2372;
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                                                                                                                                                                                                                 Gaps
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Sequence 33, Application US/09566921 Patent No. 6682888

APPLICANT: Loring,

Jeanne F.

Tingley, Debora W.

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RESULT 17
US-09-165-522-9/c
; Sequence 9, Application US/09165522
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                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-130-616-175
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US-09-130-616-175/c
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 175
LENGTH: 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 175, Application US/09130616C Patent No. 6221850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03 NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McKay, Robert A. APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAWE/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6682888 413797.7
NAWE/KEY: unsure
LOCATION: 1770-1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 98.8%;
                                                                                                                                                                               1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1570 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1510
                                                                                                                                                                                                                626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690
                                                                                                                                       686 ATTACTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
                                                                                                                                                                                                                                                    74;
                                                                                                                                                                           GCACCTGAAGGTGAGGGCTTGGCCTTTGACTACGCCGTTCTTAGTCTTCTCTTCTGAGTTC 1446
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                                                                                                   ATTACTTCCTTGTAGATGAGTTCTTT 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                      86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g, or other
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                                                                                                                                                                                                                                                                      Score 66.8; DB 3
Pred. No. 4.4e-07
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                        Length 1975;
                                                                                                                                                                                                                                                      Indels
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NAME/KEY: Coding Sequence;
LOCATION: 364...1641;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-165-522-9
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US-09-130-616-176/c
                                                                                                                      Sequence 176, Application US/09130616C Patent No. 6221850 GENERAL INFORMATION:
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Best Local :
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GENERAL INFORMATION:
APPLICANT: Davis,
                                                                                  APPLICANT: McKay, Robert A. APPLICANT: Dean, Nicholas N
                                                                 APPLICANT: Monia, Brett
                                             APPLICANT: Nero,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
PPLICANT: Nero, Pam
PPLICANT: Gaarde, William A.
ITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                  Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NNMM: Fascs 1 Defer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                            1445 ATTACTTCCTTGTAGATGAGTTCTTT 1420
                                                                                                                                                                                                                                                                                                                                   1505 GCACCTGAAGGTGAGGGCTTTGACTACGCCGTTCTTAGTCTTCTCTCTGAGTTC
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                      686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                      626 GTACCTGAAGGAGGAGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          86.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                            Score 66.8; DB 3;
Pred. No. 4.4e-07;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1975;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 19
US-09-165-522-11/c
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; ORGANISM: Mus musculus
US-09-130-616-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.1%;
Best Local Similarity 86.6%;
Matches 71; Conservative
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LENGTH: 2522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6943000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS FILE REFERENCE: ISPH-0318
                                                                                                                                        INFORMATION
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/165,522
APPLICATION NUMBER: 02-Oct-1998
PRIOR APPLICATION NUMBER: 60/060,995
PRIOR APPLICATION NUMBER: 60/060,995
PRIOR APPLICATION NUMBER: 60/060,995
PRIOR DATE: 03-OCT-1997
                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
FEATURE:
                 MOLECULE
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCTTGTAGATAAGTTCTGT 711
                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                             LENGTH: 2522 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                      TELEX: 200154
N FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitmarsh, Alan
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                                  linear
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l, Richard A.
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Pred. No. 1.9e-06;
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OTHER INFORMATION: n = A,T,C
US-09-949-016-17088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-090
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-090
                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                      Patent No. 622185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 17088
LENGTH: 48313
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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    APPLICANT: MONIA, Brett
APPLICANT: NETO, PAM
APPLICANT: Gaarde, Milliam A.
APPLICANT: Gaarde, Milliam A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                           APPLICANT: McKay, Robert A. APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(48313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 71; Conserv
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SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                            CCTTGTAGATAAGTTCTGTAAGAAAACAGCTGTGTTATTATAGAAAAACAAATTTAT 747
                                                                                                                                                                                               Application US/09130616C
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ilarity 86.6%;
Conservative
ISPH-0318
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Pred. No. 1.9e-06;
0; Mismatches 11
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; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 2372
                                                                                                                                                                                                                                                                            RESULT 23
US-09-130-616-173/c
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; ORGANISM: Homo sapiens
US-10-104-047-1930
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US-10-104-047-1930/c
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Best Local (
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SEQ ID NO 165
LENGTH: 1408
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Best Local Similarity
                                                 APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Gearde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIOE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: 15PH-0318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
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70.7%;
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Pred. No. 0.0041;
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; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 173
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-173
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                                                                ; LOCATION:
US-08-220-602B-17
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Query Match
Best Local Similarity 74.4
Matches 61; Conservative
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Best Local Similarity
Matches 61; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/220, FILING DATE: 25-MAR-1994 CLASSIFICATION: 435 ATTORNEY_AGENT INFORMATION: NAME: Haile, Ph.D., Lisa A., REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07257 TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT: I
APPLICANT: N
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: ANNING, LIN
APPLICANT: DERIJARD, BENOIT
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 25
                                                                                                                                                               TOPOLOGY: 1:
MOLECULE TYPE:
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                                                                                                                                                IMMEDIATE SOURCE:
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ADDRESSEE: FIL
ADDRESSEE: FIL
4225 F
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STATE: California
                                                                                                  NAME/KEY:
                                                                                                                               CLONE: JNK2
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DAVIS, ROGER
                                                                                                                                                                                                                                                                           (619) 678-5099
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59..1330
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25 Executive Square, Suite 1400
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                                                                                                                                                               DNA (genomic)
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                6.0%;
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; Pred. No. 0.01
0; Mismatches
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   Score 48.4; DB 3;
Pred. No. 0.017;
0; Mismatches 21;
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                                Length 1780;
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Length 1780;

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FILE REFERENCE: REGEN1120-10
CURRENT APPLICATION NUMBER: US/09/861,098A
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 08/220,602
PRIOR FILING DATE: 1994-03-25
PRIOR FILING DATE: 1994-03-25
PRIOR APPLICATION NUMBER: US 08/094,533
PRIOR FILING DATE: 1993-07-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                         Patent No. 6846644
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Patent No. 6706509
                                                                                                                                                                               APPLICANT: KARIN, Michael
APPLICANT: DAVIS, Roger
APPLICANT: HIBI, Mashiko
APPLICANT: LIN, Anning
APPLICANT: LIN, Anning
APPLICANT: DERIJARD, Benoit
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                   -09-861-098A-17/c
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APPLICANT: DERIJARD, Benoit
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
FILE REFERENCE: REGEN1120-12
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ORGANISM: Homo sapiens
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LOCATION: (59)..(1330)
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HIBI, Masahiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09861012A
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74.4%;
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Pred. No. 0.017;
0; Mismatches 21;
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US-09-861-097-17/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Applicati
Patent No. 6863888
GENERAL INFORMATION:
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LENGTH: 1780
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Best Local Similarity
                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/220,602
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.,
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/015001 (PD3205)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASAHIKO, HIBI
ANNING, LIN
DERIJARD, BENOIT
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible operating system: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, V CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,097
FILING DATE: 18-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                           FEATURE:
                                                            IMMEDIATE SOURCE:
CLONE: JNK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH &
STREET: 4225 Execu
                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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    NAME/KEY:
LOCATION:
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                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                            TELEPHONE: (619)
TELEFAX: (619) 67
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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    CDS
59..1330
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Pred. No. 0.017;
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; NAME/KEY: CDS
; LOCATION: 59..1330
PCT-US94-12913A-17
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PCT-US94-12913A-17/c
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Query Match
Best Local Similarity
Matches 61; Conserv
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Best Local Similarity 74.4%;
Matches 61; Conservative
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                                                                                                                                                                                                                                                TELEFAX: (619) 455-5110
NFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1780 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 9006,

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: PCT/US94/12913A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lin, Anning
APPLICANT: Derijard, Benoit
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/I
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                           IMMEDIATE SOURCE:
CLONE: JNK2
                                                                                                                                                                          TOPOLOGY: linear OLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     NAME: LISA A. HAILE, PH.D. REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUDRESSEE: Spensley Horn Jubas & Lubitz STREET: 1880 Century Park East, Suite 500 CITY: Los Angeles STATE: California COLMENS.
                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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   Conservative
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Davis, Roger
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                                                                                                                                                                                                                                                                                                                     (619) 455-5100
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                  74.4%;
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 Score 48.4; DB 7; Length 1780; Pred. No. 0.017; O; Mismatches 21; Indels 0
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Pred. No. 0.017;
0; Mismatches 21;
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RESULT 30
US-09-130-616-169/c
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                                   US-09-130-616-169
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                                                                                          SEQ ID NO 169
LENGTH: 1782
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 169, Application US/09130616C Patent No. 6221850
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                               APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
FULCATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (59)..(1333)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L31951/Genbank
DATABASE ENTRY DATE: 1994-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Monia, Brett P.

APPLICANT: Xu, Xiaoxing S.

TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR

TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
                                                                                                                             NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                      APPLICANT: Monia,
                                                                                                                                                                                                                                                                                                                                      APPLICANT: McKay, Robert A. APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: ISPH-0336
CURRENT APPLICATION NUMBER: US/09/209,668A
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1782
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 6.0%;
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Pred. No. 0.01
0; Mismatches
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 Score 48.4;
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Length 1782;
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                                                                                                                GENERAL INFORMATION:
APPLICANT: MCKAY, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Mero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISH-0318
                                                                                                                                                                                                                                                                                                            Sequence 171, Application US/09130616C Patent No. 6221850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 13750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13750, Appl Patent No. 6812339 GENERAL INFORMATION:
SEQ ID NO 171
           CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03 NUMBER: OF SEQ ID NOS: 178
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(132456)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             126528 AACTTCCTTATATATCAATTCTGTAAAAGA 126499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                688 TACTTCCTTGTAGATAAGTTCTGTAAGAAA 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%;
Similarity 71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTCAT 687
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Pred. No. 0.055;
0; Mismatches · 26;
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0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 132456;
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 91463128
US-09-023-655-953
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                                           Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                           SOFTWARE: World Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REFERENCE/DOCKET NUMBER: 9A-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6607879
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Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                                                                                                 TELEFAX: (650) 845-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1392
TYPE: DNA
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suman G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                   Conservative
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77.0%;
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                                                  Score 46.8; DB 3;
Pred. No. 0.041;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46.8; DB Pred. No. 0.041;
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                                                                                 Length 1392;
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                                                     Indels
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; LENGTH: 1523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-172
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; ORGANISM: Human
US-09-949-016-5346
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                       NUMBER OF SEQ ID NOS:
SEQ ID NO 172
                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6221850
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5346
LENGTH: 1392
   Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 172, Application US/09130616C
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Best Local S
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APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: GAARDE, ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5346, Application US/09949016
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03
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Similarity 77.0%;
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     Conservative
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                   5.8%;
77.0%;
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   0,
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 Score 46.8; DB 3; Length 1523; Pred. No. 0.042; o; Mismatches 17; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
Gaps
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RESULT 37
US-09-016-434-1437/c
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             Sequence 1437, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.8%;
Best Local Similarity 77.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-UUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: WII-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 1769 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 60 SI
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                    698 TAGATAAGTTCTGT 711
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                                                                                                                                                                                                                               TAAATTAGCTCTTT
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60 State Street
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Pred. No. 0.043;
0; Mismatches
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; CLONE: 9607785
US-09-016-434-1437
                                                                                                                                                                                                                                                                                                                          US-09-949-016-53117/c
                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 53117
LENGTH: 601
                                                                                                                                                                                                                                                                                      Sequence 53117, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
[NFORMATION FOR SEQ ID NO: 143
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UJ
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TOPOLOGY: lines
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1873 base pairs TYPE: nucleic acid
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; FEATURE:
; NAME/KEY: promoter;
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t.,
US-09-806-708B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Applica Patent No. 6784342 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
377
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                                                                                                                                                                                                                                                                                                                                                      137 TAGATTCTGTGGCTAGCAAACGAAAATTTTCCAAGCTGACCTTAACCGGAGCCCATCTT 196
                                                                                                                                                                                                                                                                                                                                                                                                   175 WDDDTKYHMWNNNGCBTVTWMVRYKTDRDWSBKRMNYGMBWWKNWSYDVTYYWWVWDDMC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 TNKWGKTGWRHRYWRWRAMBDTVDHHYVTAMNNAWTTMCMMDKDDKRTRWWWKKNNNATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519 AATACTTTTAAATTGTTTTTTAAACATTTTTACACATGAAAAATATCTTTTTCTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 ATTACTATTAAAATTATTATGAAAAAGTTTTTGTCCTGGATCATTACCATCAGAATAAT 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WKMDMDWBGTYNNNNNGGRTYYGWTKNKKMWTYYKWKANNCKWRAWDHKTCTHNNTTWWK
TCTTCAGGATTCATTACTATTAAAATTATTTATGAAAAAGTTTTTGTCCTGGATCATTAC 436
                                                                                                                                 WTYKKARHBARWDWVWHSAWKKWHANAAHYSRKKWTBYKRKTMVNNNNGTTMWKRMWAWY 414
                                                                                                                                                                                                                       WGWNRABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNNNNN 354
                                                                                                                                                                                                                                                                  GGTAGATGTTTCAACTATTGTCACATCAACCTTGAGAAGAGTTCAAACACTAAGAATGAA
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                                                                                  GGGCATTATGGCTCTGAATTTTGATGAGGCACATTTACCCTTTAGCCCATGTTAACATTT 376
                                                                                                                                                                        TGAGGGAAGAGGTAGCGGCTGAAAGGATTACTGAGCTCCACATTGACTTGATGGTCAAAA 316
                                                                                                                                                                                                                                                                                                            KRKVRRWVRTRGRMRNYMVÄWBTÄHRRRYNNGWTBAMAYRRWTMNNNNNÄKAMCKRAKY 294
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ilarity 11.0%; Pred. No. 0.061;
Conservative 284; Mismatches 400;
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TITLE OF INVENTION: Regulation of Embryonic T
FILE REFERENCE: 4810-59741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
SEQ ID NO 22
LENGTH: 1141
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US-09-806-708B-22/c
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Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic T
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311
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                                                                                                                                                                        191 CATCTTGGTAGATGTTTCAACTATTGTCACATCAACCTTGAGAAGAGTTCAAACACTAAG
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                                       948 TAGKMCNNNNNWTTDVRRMAMKAKNNNNNNAYWTACYNRAATNNKMATHWMKWTHGAHS
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                                                                                                                                                                                                                                                                                                                                                        71
                                                                                 AATGAATGAGGGAAGAGGTAGCGGCTGAAAGGATTACTGAGCTCCACATTGACTTGATGG
                                                                                                                                                                                                                  RWCMRTYAMRTWYTRSNANWSCATKBMWWTMKWYATKYRTAWYAMWCAWRNNNMWCATNG 1009
                                                                                                                                                                                                                                                                GTGTATTAGATTCTGTGGCTAGCAAACGAAAAATTTTCCAAGCTGACCTTAACCGGAGCC
                                                                                                                                                                                                                                                                                                          TKTKTYKKANNNNNNNGMGKDWNRMDATKWSATGTAWWTNHAKRGATMCWYWYWTGTNR 1069
                                                                                                                                                                                                                                                                                                                                                 TCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCACATTTACCCCTTTAGCCCATGTTA 370
                                                                                                                            YAKSCATNNAMWYATTRWAAYAAAKWARWAGNNMRMYGAAAGNKWGCMAAMATMGBWWAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACAAATTTATCCTTCATCCACAGGGAAATTCATTACTTAATGCCAAATA 786
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11.9%; Pred. No. 0.061;
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                                                                                                                                                                                           ; FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (1)...(100877)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-13276
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US-09-949-016-13276
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 13276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13276,
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                    14071
                                           389 ATTACTATTAAAATTATTATGAAAAAGTTTTTGTCCTGGATCATTACCATCAGAATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 828 TWWABWKHSWCNNNNNNNNNNNNNNWCHYTTANABBCYRANNNNAAARMARTCNNYMHA 769
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                    AATACTTTTTAAATTGTTTTTTAAACATTTTTACACATGAAAAATATCTTTTTCTACAT 14130
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Properties Genser. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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US-09-949-016-53116
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FI
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Patent No. 6639063
GENERAL INFORMATION:
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-09-621-976-2813
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                      NAME/KEY: CDS
LOCATION: 235
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                      ..399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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OF DETECTION AND USES THEREOF
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: McMia. Brett
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 178
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 168, Application US/09130616C Patent No. 6221850 GENERAL INFORMATION:
                                                                                                                                            Query Match 5.5%;
Best Local Similarity 69.8%;
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                     LENGTH: 1349
TYPE: DNA
ORGANISM: Homo sapiens
1095
                                 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 ATATTTTGTYYWTWWKTWWYWTTYTWTRMWWMKKKARRWYYWWKSTYACASRYRKYTWGW 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 ACACTGAATATCAAAAGAAATAAAACTAAAATCATTATAAGGACACAACCATGTGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 17.7
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATCCACAGG
ATAACTICCTTATATATCAATTCTTT 1070
                                 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                         GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRRTMMMWGYRYWWRKKSYRRTRCAWAYAWKTK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATTCATTACTTAATGCCAAATAATTACGTT 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYKKGSTYWTMKCTCATWCYWYWKYWKRMWSKTCWSGSRGGYMTSYTSTRSYSMYWASWM
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                                                                        GCACCTAAAGGAGAGGGCTGCCCCCGTATAACTCCAT
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17.7%;
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                                                                                                                                            Score 44.4; DB
Pred. No. 0.16;
0; Mismatches
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                                                                                                                                                26;
                                                                                                                                                                                   Length 1349;
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                                                                                                                                                Indels
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WS-09-130-616-166/c
US-09-130-616-166/c
; Sequence 166, Application
; Patent No. 6221850
; GENERAL INFORMATION:

US/09130616C

APPLICANT: McKay, Robert

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                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NVMBER: HORPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NVMBER: US/09/016.434

FILING DATE: HERFWITTH
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Patent No. 650093
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LENGTH: 1365
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: JOHNSON TOMBOSTTION
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                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1139
SEQUENCE CHARACTERISTICS:
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APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gearde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                     NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: PALO ALTO
STATE: CALIFORNIA
STRANDEDNESS:
                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                 ENGTH:
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ucleic acid
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Pred. No. 0.16;
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; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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US-09-621-976-2813
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SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GENBANK CLONE: g1463130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1154 GCACCTANAGGAGAGGGCTGCCCCCGTATAACTCCATTCTTGGTTCTCCTCCCAAGTCC
385
                             413
                                                                325
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                                                                                                                                                                                                  205
                                                                                                                                                                                                                                  233 AAGAGTTCAAACACTAAGAATGAATGAGGGAAGAGGTAGCGGCTGAAAGGATTACTGAGC
                                                                                                                                                                                                                                                                   145 KRWKKAWTTWWWKKTYYWAATRYWWMMCWTKRWRASWWYCWWWGKARKWSTWRKSRSYAS
                                                                                                                                                                                                                                                                                                                                                                    123 GCACAATTGTGTATTAGATTCTGTGGCTAGCAAACGAAAAATTTTCCAAGCTGACCTTAA 182
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                                                           RASMWWRRWYYTMMKWWKYAWARAAWRWWAMWAWRRACAAAATATAATTATTTATGGT 384
                                                                                                                                                               TCCACATTGACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCACATTT
                                                                                                                                                                                                 ARSAKRCCYSCSWGAMSWKYMWRMWRWRGWATGAGMKAWRASCMMRRKYAGKSKTSYKSM
                                                                                                                                                                                                                                                                                                     CCGGAGCCCATCTTGGTAGATGTTTCA-----ACTATTGTCACATCAACCTTGAG
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ACAATTCTTGTACTTTAGCA 404
                                                                                              WMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYMWKRWWWCWARMYRYSTGT
                             AAAGTTTTTGTCCTGGATCA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.3%; Score 42.4; DB
nilarity 16.6%; Pred. No. 0.45;
Conservative 153; Mismatches
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; ORGANISM: Homo sapiens
US-09-130-616-167
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US-09-130-616-167/c
                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PA
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Patent No. 6114517
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Best Local Similarity
Matches 57; Conserv
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LENGTH: 1311
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                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION M
FILE REFERENCE: ISPH-0336
                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(1173)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L26318/Genbank
DATABASE ENTRY DATE: 1994-04-25
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/209,668A CURRENT FILING DATE: 1998-12-10 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: GABARDE OLIGONUCLEOTIDE
TITLE OF INVENTION: FOR THE MODULATION OF JNK
FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-209-668-14/c
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                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          ENGTH: 1418
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1156 CTAAAGGAGAGGGCTGCCCCCGTATAACTCCATTCTTGGTTCTCTCCTCCAAGTCCATAA 1097
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                     630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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Pred. No. 0.63;
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; SEQ ID NO 164
; LENGTH: 1418
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-130-616-164
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Search completed: July 19, 2006, 20:14:12 Job time: 207 secs
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Best Local Similarity 69.5%;
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 622185
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE TITLE OF INVENTION: FOR THE MODULATION OF JNK FILE REFERNCE: ISPH-0318 CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 BARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MCKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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US-09-925-065A-683711

US-09-925-065A-683711

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US-09-925-065A-44644

US-09-925-065A-44644

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Sequence 44644, A
Sequence 145842,
Sequence 145882,
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Sequence 1752291,
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Sequence 1, Appli
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being printed,
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US-10-450-763-29386
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US-10-450-763-11488
US-09-999-650A-22
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Sequence 2, Application US/10723681

Publication No. US20050192239A1

GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: BRAUN, ANDREAS
APPLICANT: REMAUN, MATTHEW ROBERTS
APPLICANT: REMAUN, METHODS FOR IDENTIFYING RISK OF BREITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREITLE OF INVENTION UMBER: US/10/723,681

CURRENT APPLICATION NUMBER: US/0/429,136

PRIOR APPLICATION NUMBER: US 60/429,136

PRIOR APPLICATION NUMBER: US 60/429,234

PRIOR APPLICATION NUMBER: US 60/490,234

PRIOR APPLICATION NUMBER: US 60/490,234
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US-10-723-681-2
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Best Local Similarity 99.9%;
Matches 799; Conservative
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ORGANISM: Homo sapiens
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                   GCCCATGTTAACATTITCTTCAGGATTCATTACTATTAAAATTATTTATGAAAAAGTTTT
                                                                                                         GACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCACATTTACCCTTTA
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US-11-019-829-75
US-11-019-829-75
US-09-925-065A-758673
US-09-925-065A-758673
US-10-221-613-396
US-09-925-065A-758672
US-09-925-065A-758672
US-11-060-756-376
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Sequence 75, Appl
Sequence 76, Appl
Sequence 758673,
Sequence 758673,
Sequence 396, App
Sequence 758672,
Sequence 758672,
Sequence 376, App
Sequence 377, App
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CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOPTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2
                                                                                                                                                                                                                                                      ; LENGTH: 110950
; TYPE: DNA
; ORGANISM: Homo s
US-10-857-780-2
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GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RITTITLE OF INVENTION: THEREOF
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; Sequence 2, Application US/10857780
; Publication No. US20050272043A1
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                                                         AATAAGTAAATTGTCTCAAGTCATACTAAAGCACATTACTAGGATCAGTAAAAAATATAT
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RESULT 3
US-09-25-065A-683710/c
US-09-25-065A 683710/c
; Sequence 683710, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE OF INVENTION: NUCLECTURE FOLYMOLPHIAMS
FILE REFERENCE: 10827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 683710
LENGTH: 2669
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   RESULT 4
US-09-925-065A-683711/c
Sequence 683711, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
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; ORGANISM: Homo sapiens
US-09-925-065A-683710
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Pred. No. 1.2e-178;
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/252,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEG ID NOS: 957086
SOPTWARE: FASTSEQ for Windows Version 4.0
SEG ID NO 683711
LENGTH: 2669
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; ORGANISM: Homo sapiens
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Best Local Similarity 99.8
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             ATTTTTAGTCTTTTCTTCTGAATTCATTACTTCCTTGTAGATAAGTTCTGTAAGAAACAG
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                                                             TTTATTGGTTATTCACGGAGAGTGAGTACCTGAAGGAGAAGGCTGTCCTTTTACTACACC
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Pred. No. 1.2e-178;
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US-09-325-065A-683712/c

Sequence 683712, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,092

PRIOR APPLICATION NUMBER: US 60/25,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: Fast-SEQ for Windows Version 4.0

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Best Local Similarity 99.8
Matches 798; Conservative
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TYPE: DNA
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                                                                      GACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCACATTTACCCTTTA
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Pred. No. 1.2e-178;
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US-09-925-065A-683710/c
US-09-925-065A-683710, Application US/09925065A
Publication No. US20050228172A9
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CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-26

PRIOR FILING DATE: 2000-11-20

PRIOR PRIOR DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/269,846

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 683710
LENGTH: 2669
                                                                                                                                                                                                                                                                                        Query Match 99.6%;
Best Local Similarity 99.8%;
Matches 798; Conservative
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-683710
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Pred. No. 1.2e-178;
0; Mismatches 2;
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Sequence 683711, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.

FITLE OF INVENTION: Identification and Mapping of Single
FITLE OF INVENTION: Nucleotide Polymorphisms in the Human General Reference: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2000-10-1-16

PRIOR FILING DATE: 2001-05-09

NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER: US 60/289,846
US-09-925-065A-683711
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                   ORGANISM: Homo sapiens
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Query Match

99.6%;

Score 796.8;

DB 5;

Length 2669;

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RESULT 8
US-09-925-065A-683712/c
Sequence 683712, Application US/09925065A
Sequence 683712, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION: David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Gen
FILE REFERENCE: 108627, 135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION UNMBER: US 60/243,096
PRIOR APPLICATION UNMBER: US 60/243,096
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0; Mismatches 2;
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PRIOR DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRANCE OF SEQ ID NO 683712
LENGTH: 2669
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Best Local Similarity 99.8%;
Matches 798; Conservative
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                                               CTGTGTTATTATAGAAAAAATTTATCCTTCATCCACAGGGAAATTCATTACTTAATGC
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Pred. No. 1.2e-178;
0; Mismatches 2;
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APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: WETHODS FOR IDENTIFYING RIS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION UNMEER: US/10/857,780
CURRENT APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-07-24
PRIOR PRIOR PRIOR DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
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RESULT 10
US-10-857-780-4943
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Best Local Similarity 99.8%;
Matches 464; Conservative
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ORGANISM: Homo sapiens
-10-857-780-4942
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APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFA
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Pred. No. 1.3e-99;
0; Mismatches 1
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PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILLING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILLING DATE: 2003-07-24
PRIOR FILLING DATE: 2003-07-24
PRIOR FILLING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: Patentin version 3.2
SEQ ID NO 4943
LENGTH: 823
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
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Best Local :
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APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILLING DATE: 2004-05-28
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CACAGGGAAATTCATTACTTAATGCCAAATAATTACGTTTTGATG
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Pred. No. 1.3e-99;
0; Mismatches 1;
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RESULT 11
US-09-925-065A-44644/c
US-09-925-065A, Application US/09925065A
; Sequence 44644, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single
 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human

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RESULT 12
US-09-925-065A-44644/c
Sequence 44644, Application US/09925065A
Publication No. US20050228172A9
Publication No. US20050228172A9
PUBLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Gence TITLE OF INVENTION Nucleotide Polymorphisms in the Human Gence TITLE OF INVENTION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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Best Local Simi
Matches 457;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44644
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-09-925-065A-44644
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Pred. No. 5.3e-98;
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 44644
LENGTH: 572
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                    AAATTCATTACTTAATGCCAAATAATTACGTTTTGATG
                                                                     AAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATCCACAGGG
                                                                                                                      CTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTACTTCCTTGTAGAT
                                                                                                                                                                      GTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGCAACCCCTACACAAAAGGCCAAG
                                                                                                                                                                                                                                                              CACTGAATATCAAAAGAAATAAAACTAAAATCATTATAAGGACACAACCATGTGATATTT
                                                                                                                                                                                                                                                                             CACTGAATATCAAAAGAAATAAAACTAAAAATCATTATAAGGACACAACCATGTGATATTT
                                                                                                      CTGTCCTTTTACTACACCATTTTTAGTCTTTTTTCTTCTGAATTCATTACTTCCTTGTAGAT
                                                                                                                                                         GTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAG
                                                                                                                                                                                                                                                                                                                 TATTTATGAAAAAGTTTTTGTRCTGGATCATTACCATCAGAATAATCAGAATGAATGCCCA
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                57.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
 115
                         800
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RESULT 13

US-10-301-480-145882/c

; Sequence 145882, Application US/10301480

; Publication No. US20060057564A1

; GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: in the Human Genome
 TITLE OF INVENTION: in the Human Genome
 FILE REFERENCE: 108827.137

; CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

prior APPLICATION NUMBER: US 10/215,598

prior APPLICATION NUMBER: US 60/311,695

prio

702

213

642 333 582 393

273

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-10
NUMBER: OS 5001-08-10
NUMBER: OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ.ID NO 759291
LENGTH: 572
                                                                                                                                                                                                                ; TYPE: DNA; Homo sapien 
; ORGANISM: Homo sapien 
US-10-301-480-759291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-301-480-759291/c
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Best Local Simi
Matches 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 759291, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                  Matches 457;
                      512
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                                                                                                                                                  57.0%; ilarity 99.8%; Conservative
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99.8%;
                                                                                                                                                Score 456.4; DB 12; Pred. No. 5.3e-98; 0; Mismatches 1;
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Pred. No. 5.3e-98;
0; Mismatches 1
                                                                                                                                                                               DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Single Nucleotide Polymorphisms
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                                                                                                                                                                              Length 572;
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APPLICANT: Fournier, Alain
APPLICANT: Maury, Isabelle
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
APPLICANT: Desanlis-Cremond, Francine
TITLE OF INVENTION: New Polypeptides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR APPLICATION NUMBER: DS/07/870/00104
PRIOR APPLICATION NUMBER: US 69/122,175
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-01-20
                                                                               RESULT 16
US-09-165-522-1/c
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; TYPE: DNA
; ORGANISM: homo sapiens
US-09-909-650A-23
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                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 84
Sequence 1, Application US/09165522
Publication No. US20030023990A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Flavell, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09909650A Patent No. US20020165386A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                  1223
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                                                                                                                                                                                                                                   _GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAATTC
                                                                                                                                                                   ATTACTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                  ATTACTTCCTTGTAGATAAGTTCTTT 1198
                                                                                                                                                                                                                  GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                              10.3%;
nilarity 97.7%;
Conservative
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Pred. No. 5.5e-09;
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Length 1422; Indels

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US-10-641-643-952/c
; Sequence 952, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                     RESULT 17
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Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Passe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/0
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                  APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                         1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 68...1459
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
· MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/165,522 FILING DATE: 02-Oct-1998 PRIOR APPLICATION DATA:
              CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             1323 GCACCTGAAGGAGAGGCTGTCCTTTTACTACACCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                           686
                                                                                                                                                                                                                                                                                                                                                                                                                 626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                         ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                        ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rakic, Pasko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.3%;
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                                                                                                          THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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Query Match
Best Local Similarity
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; SOPTWARE: PATENTIN Version 3.2
; SEO ID NO 56
; LENGTH: 1505
; TYPE: DNA
; ORCANISM: Homo sapiens
US-10-343-710-56
                                                                                                                                                                                      APPLICANT: WETZELS, Ingrid
APPLICANT: WIENT, Stephan
APPLICANT: WIENE, E
APPLICANT: SCHAEFER, M., K.-H.
INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-343-710-56/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56, Application US/103 Publication No. US20040087478A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 952: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 10.3%;
Local Similarity 97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION NUMBER: US/10/641,643

FILING DATE: 14-Aug-2003

FILING DATE: 14-Aug-2003

CLASSIFICATION: UNKnown>
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 952 :
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CLONE: 91463124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Zeller, Karen J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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10.3%;
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Pred. No. 5.6e-09;
Score 82.8; DB 8; Pred. No. 5.6e-09;
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                    Length 1505;
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                                                                        Query Match
Best Local Similarity
                                                            Matches
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                                                                                                                                                                                                                                                                                                            NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 1036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
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                                                                                                                                                                                                                                                                 TELEX: 200154

NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                         FEATURE:
                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
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APPLICANT: Yang, Di
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                  LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 225 P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTGAATTC 1264
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                                                            Conservative
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Rakic, Pasko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitmarsh, Alan
                                                                                                                                        Coding Sequence 68...1459
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                                                                         Score 82.8; DB 16
Pred. No. 5.6e-09;
                                                            Mismatches
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                                                                                        DB 16;
                                                                                       Length 1505;
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                                                            Gaps
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                                                            0,
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-817-10
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US-11-127-817-10/c
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SEQ ID NO 10
LENGTH: 2211
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Best Local Similarity
Matches 84; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT APPLICATION NUMBER: US/11/127,817
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: PatentIn version 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                 Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS
NUMBER OF SEQUENCES: 24
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APPLICATION NUMBER: US/09/165,522 FILING DATE: 02-Oct-1998 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTT
                                                                                                                                                                                          ZIP: 02110-2804
                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                            STREET: 225 Franklin Street
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10. US20050287519A1
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Whitmarsh, Alan
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Pred. No. 6.7e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15;
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Best Local Similarity 97.7%;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: FASSE, J. PETER
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
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SEQUENCE CHARACTERISTICS:
LENGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                          FILING DATE: 12-UULY-2005
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/09/165,522
FILING DATE: 02-Oct-1998
                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/11/180,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1419
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
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Flavell, kı...
Rakic, Pasko
Whitmarsh, Alan
Man, Chia-Yi
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TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                 IBM Compatible
SYSTEM: Windows 95
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                                         10363/005001
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Pred. No. 6.9e-09;
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SEQ ID NO 34
LENGTH: 2677
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/10765700 Publication No. US20050130171A1
                                                                                                                                    Matches
                                                                                                                                              Query Match
Best Local Similarity
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Best Local S
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APPLICANT: Tingley, Debora W.
APPLICANT: Tingdey, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/10/765,700
CURRENT FILING DATE: 2004-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIORT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 413797.5
                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: 2024
                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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TOPOLOGY: lir
MOLECULE TYPE:
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TELEX: 2
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1735 ATTACTTCCTTGTAGATAAGTTCTTT 1710
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                                 989
                                                                                      626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                      ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                 GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 1736
                                                                                                                                Conservative
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97.7%;
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                                                                                                                                                Score 82.8; DB 10
Pred. No. 7.3e-09;
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Pred. No. 6.9e-09;
                                                                                                                                    Mismatches
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                                                                                                                                                                  Length 2677;
                                                                                                                                    Indels
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US-11-127-817-11/c

Sequence 11, Appropriate Publication No.

Application US/11127817 No. US20050287519A1

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel

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; OTHER INFORMATION: 100% homologous to Mus musculus JNK3, accession number; OTHER INFORMATION: AB005665, Smith-Waterman Score=136.
US-10-450-763-29386
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; ORGANISM: Homo sapiens
US-11-127-817-11
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                                                                                                                                                                    Matches 81;
                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29386, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Custom
SEQ ID NO 29386
LENGTH: 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SIMILAR
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                                                                                                                                                                                             Local Similarity
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  393
                                          688 TACTTCCTTGTAGATAAGTTCT 709
                                                                                   453
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                                                                                                                              628 ACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCAT 687
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                                                                                                                                                                      Conservative
                                                                                                                                                                                        10.1%;
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                                                                                                                                                                                    Score 80.4; DB 10
Pred. No. 1.7e-08;
                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                               DB 10;
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                                                                                                                                                                      Indels
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US-10-450-763-11488
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US-10-450-763-11488/c
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US-10-450-763-2768/c
                                                                                                                                                                             ; SOFTWARE: Custo
; SEQ ID NO 11488
; LENGTH: 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11488, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
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SOFTWARE: Custom
SEQ ID NO 2768
LENGTH: 999
TYPE: DNA
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR PPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (373)...(453)
OTHER INFORMATION: 100% homologous to Mus musculus JNK3, accession number
OTHER INFORMATION: AB005665, Smith-Waterman Score=136.
                        LOCATION: (25)..(1452)
OTHER INFORMATION: 81% homologous to Homo sapiens putative p150, accession number
OTHER INFORMATION: U93572, Smith-Waterman Score=1883.
                                                                                         NAME/KEY: SIMILAR
                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                               TYPE: DNA
                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393
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                                                                                                                                                                                                                                  Custom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Query Match

10.1%;

Score 80.4;

DB 10; Length 1111;

Matches

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889

RESULT 28

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APPLICANT: Zhou-Liu, Qing
APPLICANT: Desanlis-Cremond, Francine
TITLE OF INVENTION: New Polypetides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 199-01-26
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                    US-09-165-522-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: homo sapiens
US-09-909-650A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-909-650A-22/c
                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09165522 Publication No. US20030023990A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 29.
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application U Patent No. US20020165386A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Aventis Pharmaceuticals Inc APPLICANT: Fournier, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1306
                                                                                                                             Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                 AL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT Flavell, Richar
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1219 CTTCCTTGTAGATAAGTTCTTT 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690 CTTCCTTGTAGATAAGTTCTGT 711
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COUNTRY: USA
ZIP: 02110-2804
                                    STATE: MA
                                                       CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maury, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fournier, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09909650A
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                                                                                                                                                                                                                         Whitmarsh, Alan
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                                                                                                                                                                                                                                                             Richard A.
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Pred. No. 2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1306;
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                                                                                           PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
SEQ ID NO 54
LENGTH: 1773
TYPE: DNA
ORGANISM: Homo sapiens
US-10-343-710-54
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                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WNENDT, Stephan
              Query Match 10.1%; Score 80.4; DB 8; Best Local Similarity 98.8%; Pred. No. 2.2e-08; Matches 81; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54, Application US/10343710 Publication No. US20040087478A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/343,710 CURRENT FILING DATE: 2003-09-17
                                                                                                                                                                                                                                                                                                                         APPLICANT: WEIHE, E. APPLICANT: SCHAEFER, M., K.-H. TITLE OF INVENTION: SCREENING METHOD FILE REFERENCE: 029310.52022US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: FastSEQ for WINDOWS Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-0cc-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1283 CTTCCTTGTAGATAAGTTCTTT 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1343 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1284
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
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Pred. No. 2.2e-08;
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US-11-180-044-4
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                                                                                                 Query Match
Best Local Similarity
Matches 81; Conserv
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                                                                                                                                                                                                                                                                                                 TELEX: 200154
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                            LOBOTOGA:
                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fasse, J. Peter REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                          1343 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTTCTTGAATTCATTA 1284
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690 CTTCCTTGTAGATAAGTTCTGT 711
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EDNESS: double
                                                                   CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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Yang, Di
                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
SYSTEM: Windows 95
FastSEQ for Windows Version 2.0b
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                                                                                                                                                                     Coding Sequence 92...1357
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Fish & Richardson P.C.
                                                                                                                                                                                                                 DNA
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                                                                                                             10.1%;
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                                                                                                                                                                                                                                                                                                                                                                                  32,983
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                                                                                                Score 80.4; DB 16
Pred. No. 2.2e-08;
0; Mismatches 1
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                                                                                                                             DB 16;
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RESULT 33
US-09-771-161A-87/c
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Best Local S
Matches 81
                                                                                                                                                                       SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 87, Application US/09771161A Patent No. US20020110811A1
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Publication No. US20050196754A1
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 800620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-10
PRIOR APPLICATION UNMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                              LENGTH: 21
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 790CIP3/US
NAME/KEY: -
LOCATION: (1)..(2131)
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1563)..(1688)
OTHER INFORMATION: 80% homologous to Homo sapiens Human secreted protein, SEQ ID
OTHER INFORMATION: NO: 7131,accession number G03050,Smith-Waterman Score=173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1283 CTTCCTTGTAGATAAGTTCTTT 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 TACTTCCTTGTAGATAAGTTCT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 AGCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 ACCTGAAGGAGAAGGCTGTCCTTTTACTACACCAT
                                                                                                                                                    2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                           PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTTCCTTGTAGATAAGTTCT 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                version 3.0
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Pred. No. 2.3e-08;
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                      'g' or 't'
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Matches

RESULT 34

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RESULT 35
US-09-165-522-6/c
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; ORGANISM: Homo sapiens
US-11-127-817-12
                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09165522 Publication No. US20030023990A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 2155
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/111 Publication No. US20050287519A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/127,817 CURRENT FILING DATE: 2005-05-12 PRIOR APPLICATION NUMBER: 60/570,352 PRIOR FILING DATE: 2004-05-12 PRIOR APPLICATION NUMBER: 60/603,948 PRIOR FILING DATE: 2004-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad
APPLICANT: Laenen, Wendy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 534
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COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                  APPLICANT: Davis, Roger J.
Flavell, Richard A.
Rakic, Pasko
                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                           Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1198 CTTCCTTGTAGATAAGTTCTTT 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            690 CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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                                                               STATE: MA
                                                                                                         STREET: 225 Franklin Street
                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/11127817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                     Whitmarsh, Alan
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Pred. No. 2.5e-08;
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Pred. No. 2.4e-08;
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, Sequence 7, Application US/09165522
; Publication No. US20030023990A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 81; Conserv
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INFORMATION FOR SEQ ID NO: 6:
                                                      COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Mindows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION NUMBER: US/09/165,522
APPLICATION NUMBER: US/09/165,522
PILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
  APPLICATION NUMBER: 60/060,995 FILING DATE: 03-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Davis, Roger J. Flavell, Richar
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/060,995 FILING DATE: 03-OCT-1997 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/165,522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-Oct-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690
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                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: MA
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rakic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuan, Chia-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.1%; Score 80.4; DB 3; 98.8%; Pred. No. 2.6e-08; vative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10363/005001
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GENERAL INFORMATION

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LOCATION: 224...1489;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-165-522-7
                             RESULT 38
US-10-466-162-5/c
                                                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g468150
US-10-305-720-1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ફ
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Sequence 5, Application US/10466162 Publication No. US20050170343A1
                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1389, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1389
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2372
TYPE: DNA
CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                  1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1475 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1416
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                                                                                                                                                                                                 630
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                                                                                                                                                                                                                                   81;
                                                                                                                                                                                  CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTCATTA 689
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                                                                                                                               CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                CTTCCTTGTAGATAAGTTCTTT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fasse, J. Peter
REGISTRATION NUMBER:
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Pred. No. 2.6e
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Pred. No. 2.6e-08;
0; Mismatches 1
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; SEQ ID NO 5
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-466-162-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-723-681-9/c
                                                         PRIOR APPLICATION NUMBER: US 60/490,234
PRIOR FILING DATE: 2003-07-24
NUMBER OF SEQ ID NOS: 835
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10723681 Publication No. US20050192239A1
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Best Local Similarity
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                                                                                                                                                              FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/723,681
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: US 60/429,136
PRIOR FILING DATE: 2002-11-25
                                                                                                                                                                                                                                                                 APPLICANT: KAMMERER, STEFAN M.
APPLICANT: RENELAND, RIKARD
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND
TITLE OF INVENTION: TREATMENTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 76
LENGTH: 2372
TYPB: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2001-01-12
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PRIOR FILING DATE: 2001-01-12
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PRIOR APPLICATION NUMBER: US 60/261,694
PRIOR FILING DATE: 2001-01-12
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CURRENT FILING DATE: 2003-07-11
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FILING DATE: 2001-01-12
APPLICATION NUMBER: US
FILING DATE: 2001-01-12
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APPLICATION NUMBER: US
FILING DATE: 2001-01-12
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NELSON, MATTHEW ROBERTS
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US-11-127-817-9/c
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CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
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Best Local Similarity
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SEQ ID NO 11
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Best Local Similarity
                                                                                                                                                                                              Sequence 9, Application US/11127817
Publication No. US20050287519A1
                                                                                                                                                                                GENERAL INFORMATION:
  APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
                                                                                                                APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: WETHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: THEREOF
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 2.6e-08;
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Best Local
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RESULT 42
US-11-180-044-6/c
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SEQ ID NO 9
LENGTH: 2372
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                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2004-08-24
                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kuan, Chi
APPLICANT: Yang, Di
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                      TELEPHONE:
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225 Franklin Street
                                                                                                        617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
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Chia-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roger J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JNK3 MODULATORS AND METHODS OF USE
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RESULT 43
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Publication No. US20060035303A1
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Best Local Similarity 98. Matches 81; Conservative
                                Query Match
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                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
                                                                                                                                                                                                                                                                            NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOTTWARE: FASTSEO for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILLING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                NAME/KEY:
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                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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                                                                                OCATION:
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225 Franklin Street
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Yang, Di
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Whitmarsh, Alan
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Flavell, Richard A.
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                                                                                Coding Sequence 224...1489
                                                                                                                                                  linear
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             10.1%; Score 80.4;
98.8%; Pred. No. 2.
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Pred. No. 2.6e-08;
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             6e-08;
                             DB 16; Length 2372;
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US-09-776-167A-8
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US-09-776-167A-8/c
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GENERAL INFORMATION:
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Best Local Similarity
Matches 81; Conserv
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LENGTH: 2982
Query Match
                                                                                                      SEQ ID NO 8
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                                                                                                                   APPLICANT: Jarnigan, Kurt
APPLICANT: Greene, Amy
APPLICANT: Greene, Amy
ITTLE ORIVENTION: RAPID, PARALLEL IDENTIFICATION OF CELL LINES
FILE REFERENCE: 0024.US
CURRENT APPLICATION NUMBER: US/09/776,167A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: USSN 60/179,893
PRIOR PILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
                                         TYPE: DNA
ORGANISM: pfastFind-JNK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/765,700
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIORT FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: 1770-1816
OTHER INFORMATION: a,
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 413797.7
                                                                                    ENGTH: 8750
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10.1%;
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Score 80.4;
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DB
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ω
••
Length 8750;
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AM101086); CURRENT APPLICATION UNWBER: US/11/136,527; CURRENT FILING DATE: 2005-05-25 PRIOR APPLICATION NUMBER: US 60/574,294; PRIOR FILING DATE: 2005-05-26; NUMBER OF SEQ ID NOS: 362830 SOFTWARE: PatentIn version 3.2

SEQ ID NO 4334
LENGTH. 7.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-165-522-9/c
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US-11-136-527-4334/c
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09165522
Publication No. US20030023990A1
GENERAL INFORMATION:
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nes 74; Conserv
COMPUTER READABLE FORM:
. MEDIUM TYPE: Diskette
. COMPUTER: IBM Compasible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
                                                                                                                                                                Whitmarsh, Alan
Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Davis, Roger J. Flavell, Richard
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                                                                                                                               COUNTRY: USA
ZIP: 02110-2804
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Pred. No. 2.4e-05;
Nismatches 12;
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0; Mismatches 1;
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; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-343-710-60
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US-10-343-710-60/c
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
CURRENT PELICATION NUMBER: PCT/EP01/09011
PRIOR PELING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTMARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WNENDT, Stephar
APPLICANT: WEIHE, E.
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WEIHE, E.
APPLICANT: SCHAEFER, M., K.-H.
TITLE OF INVENTION: SCREENING WETHOD
FILE REFERENCE: 029310.52022US
                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                             1505 GCACCTGAAGGTGAGGGCTGGCCTTTGACTACGCCGTTCTTAGTCTTCTTCTTGAGTTC 1446
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SEQUENCE DESCRIPTION: SEQ ID NO:
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/060,995 FILING DATE: 03-OCT-1997 ATTORNEY/AGENT INFORMATION:
     1445 ATTACTTCCTTGTAGATGAGTTCTTT 1420
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Pred. No. 46
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US-11-180-044-9
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Best Local Similarity 86.0
Matches 74; Conservative
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SOFTWARE: FASESEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION UNUBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REGISTRATION INFORMATION:
TELEPHONE: 617/542-8906
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/11180044 Publication No. US20060035303A1 GENERAL INFORMATION:
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COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
SOFTWARE: FASTSEQ for Wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                  1505 GCACCTGAAGGTGAGGGCTTGGCCTTTGACTACGCCGTTCTTAGTCTTCTTCTGAGTTC 1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuan, Chia-Yi
Yang, Di
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Flavell, Richard A.
Rakic, Pasko
                                                                                                                                                                                                                                                                                                                                                                       Coding Sequence 364...1641
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Search completed: July 19, 2006, 23:05:29
Job time: 1478 secs
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Best Local Similarity
Matches 74; Conserv
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LENGTH: 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rattus norvegicus
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                                                                                   1445
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Pred. No. 4e-05;
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S-11-266-748A-392414
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US-11-266-748A-223967/c
                                                                                                                                                                       Sequence 292324, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jöhnston, Patrick
APPLICANT: Wulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319.89)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo Sapiens
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APPLICATION NUMBER: US 60/662,276
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US-10-517-441-668
US-11-216-545-2975
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RESULT 3
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; Sequence 343753, Application US/11266748A
; Publication No. US20060134663A1
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US-11-266-748A-292324
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
                                                                                                                                           NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
SEQ ID NO 343753
Query Match
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SEQ ID NO 292324
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
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                                                                   TYPE: DNA
ORGANISM: Homo Sapiens
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NUMBER OF SEQ ID NOS: 483996
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Local Similarity 97.7%;
es 84; Conservative
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  Score 82.8;
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  DB 8;
  Length 1000;
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US-11-266-748A-403980/c
; Sequence 403980, Application US/11266748A
; Publication No. US20060134663A1
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US-11-266-748A-403979/c
US-11-266-748A-403979, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-403979
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Best Local
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Matches 84; Conservative
                                                          APPLICANT: Harkin, Paul
APPLICANT: Johnston, F
APPLICANT: Mulligan, K
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
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NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: EP 04105479.2
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105483.4
FILING DATE: 2004-11-03
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Mulligan, Karl
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Mulligan, Karl
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Pred. No. 1.3e-10;
0; Mismatches 2;
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RESULT 6
US-11-266-748A-475025
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CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PRICING NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PRICING DATE: 2004-11-03
                NUMBER OF SEQ ID NO
SOFTWARE: Patentin
SEQ ID NO 475025
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                                                                       PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 463996
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105483.4
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
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CURRENT FILING DATE: 2005-11-03
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; ORGANISM: Homo Sapiens
US-11-266-748A-475026
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US-11-266-748A-475025
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PELICATION NUMBER: EP 04105484.2
                                         Sequence 57178, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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APPLICANT: Johnston, I
APPLICANT: Mulligan, F
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Mulligan, Karl
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Pred. No. 1.3e-10;
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TITLE OF INVENTION: Transcriptome Microarray Tech.
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
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; ORGANISM: Homo Sapiens
US-11-266-748A-57178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 2211
                                                                                                                                                                                                                                                          Local Similarity
1263 ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                   686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                        626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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US-11-266-748A-31164/c
Sequence 31164, Application US/11266748A
Publication No. US20066134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18

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; ORGANISM: Homo Sapiens
US-11-266-748A-31164
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NIMMER OF STATE: 2005-07-18
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                    NAME/KEY: misc feature LOCATION: (1979)..(2028) OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: EP 04105483.4
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LOCATION: (161)..(201)
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 3232
                                                                                              Local Similarity
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GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTC
                                    GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAATTC 685
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Mulligan, Karl
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Pred. No. 1.7e-10;
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RESULT 12
US-11-266-748A-432957
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NAME/KEY: misc feature
LOCATION: (1979)..(2028)
OTHER INFORMATION: n is a,
US-11-266-748A-382414
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; Sequence 382414, Application US/11266748A
; Publication No. US20060134663A1
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                                                                                                   Sequence 432957, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local Similarity
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                                       APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patr
APPLICANT: Mulligan, Karl
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Transcriptome Microarray Technology TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NAME/KEY: misc feature
LOCATION: (161)..(201)
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Mulligan, Karl
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  Transcriptome Microarray Technology and Methods of Using the Same
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1.8e-10;
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CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03 PRIOR APPLICATION NUMBER: EP 04105479.2

FILE REFERENCE: 55815-0102 (319189)

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APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.7
PRIOR APPLICATION NUMBER: EP 04105485.6
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; LOCATION: (3032)..(3072)
; OTHER INFORMATION: n is a, c,
US-11-266-748A-432957
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Publication No. US20060134663A1
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: EP 04105482.6
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                                            APPLICATION NUMBER: EP 04105485.9
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APPLICATION NUMBER: EP 04105507.0
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NUMBER: EP 04105484.2
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; ORGANISM: Homo Sapiens
US-11-266-748A-403999
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; Sequence 403999, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-46908
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SEQ ID NO 46908
LENGTH: 801
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Matches 62; Conserv
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SOFTWARE: PatentIn version 3
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CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION UNUBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR APPLICATION NUMBER: EP 04105484.2
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PRIOR FILING DATE: 2004-11-03
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185
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Mulligan, Karl
                                                                       CIGCATCTGAAGGCTGATCTTTTACAACACCCATTCTTGCTTCTTTCCCAATCCATGA 186
                                                                                                                CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
CTTCTTTGTAAATTAGCTCTTT 164
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Pred. No. 0.011;
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
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; ORGANISM: Homo Sapiens
US-11-266-748A-475045
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PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-3
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105507.0
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Pred. No. 0.
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR PPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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                                                                                                                            Query Match
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LENGTH: 1180
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PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                 Local Similarity
nes 61; Conserv
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mes 61; Conserv
                                  630 CTGAAGGAGGAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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690 CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                 Score 48.4; DB Pred. No. 0.03; Mismatches
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                                                                                                                        DB 8;
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690 CTTCCTTGTAGATAAGTTCTGT

711

CTTCTTTGTAAATTAGCTCTTT 350

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APPLICANT: Markin, Paul
APPLICANT: Markin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
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US-11-266-748A-349487/c
US-11-266-748A-349487, Application US/11266748A; Sequence 349487, US20060134663A1; GENERAL INFORMATION:
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; ORGANISM: Homo Sapiens
US-11-266-748A-122015
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 04105485.9 FILING DATE: 2004-11-03
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; ORGANISM: Homo Sapiens
US-11-266-748A-432866
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US-11-266-748A-349487
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PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
                                                                                                                                                                                  SOFTWARE: PatentIn version 3.3 SEQ ID NO 432866
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                       Query Match
Best Local Similarity
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 55815-0102 (31198)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION TOMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same
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                                                                                                                                          TYPE: DNA
                                                                                                                                                               ENGTH:
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Local Similarity 74.4%;
es 61; Conservative
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Mulligan, Karl
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                       6.0%;
Score 48.4; DB 8;
Pred. No. 0.035;
0; Mismatches 21;
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                                             Length 1928;
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Conservative

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; NAME/KEY: CDS
; LCCATION: (50)...(1324)
; OTHER INFORMATION: JNK2 variant 4
US-11-283-329-231
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US-11-283-329-231/c
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; OTHER INFORMATION: JNK2 variant 1
US-11-283-329-225
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US-11-283-329-225/c
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SEQ ID NO 225
LENGTH: 1942
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GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
                                                                                                                                          SOFTWARE: Fa
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Sequence 231, Application US/11283329 Publication No. US20060134670A1
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Best Local
                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
                                                                                                                                                                                                                                                                                 APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
                                                                                                                                                                                                                                                                    FILE REFERENCE: ACADIA.043A
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NUMBER OF SEQ ID NOS: 242
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                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
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                                                                      FEATURE:
                                                                                                                        ENGTH: 1942
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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US-11-266-748A-242782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: Homo Sapiens US-11-266-748A-182241
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US-11-266-748A-182241/c
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Sequence 242782, Application US/11266748A publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul APPLICANT: Johnston, Patrick APPLICANT: Mulligan, Karl TITLE OF INVENTION: Transcriptome Microal TITLE OF INVENTION: Methods of Using the
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 182241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 61; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2005-07-18 NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR APPLICATION NUMBER: US 60/700,293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2251
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  Transcriptome Microarray Technology Methods of Using the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-242782
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 227
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Publication No. US20060134670A1
GENERAL INFORMATION:
                                                                                              Query Match
Best Local
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CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS FILE REFERENCE: ACADIA.043A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Piu, Fabrice
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                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1198)
OTHER INFORMATION: JNK2 variant 2
                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                      LENGTH: 1947
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                               .638 GAAGGCIGICCTITIACIACACCAITITIAGICTITITCTICTGAATICATITACTITCCTIG 697
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Similarity 74.4%;
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                                                                               Conservative
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                                                                             Mismatches
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                                                                                                                   DB 8;
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                                                                                                                   Length 1947;
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US-11-283-329-217/c
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US-11-283-329-229/c
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                                                                                                                                                                                                                                                                                                                 Sequence 217, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
FILE REFERENCE: ACADIA.043A
FULE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 229
LENGTH: 1947
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Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
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                                     Matches
                                   Best Local Similarity Matches 60; Conserv
                                                                         Query Match
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
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                                                                                                                            NAME/KEY: CDS
LOCATION: (18)...(1301)
OTHER INFORMATION: JNK1 variant 1
                                                                                                                                                                                                                          LENGTH: 1412
TYPE: DNA
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                                                                                                                                                                                                        ORGANISM: Homo
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OTHER INFORMATION: JNK2 variant
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626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
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                                     Conservative
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                                                   Score 44.4; DB 8;
Pred. No. 0.29;
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                                     Mismatches
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US-10-449-902-24462
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US-11-283-329-223/c
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Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 223
                                                                                                                                       SEQ ID NO 24462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 223, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
      TYPE: DNA
ORGANISM: OTYZA SALIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK099904
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver 2.1
                                                                                                                                                                                                                                                                               APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
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TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: JNK1 variant 4
                                                                                                                    LENGTH: . 1676
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o. US20060134670A1
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
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US-11-266-748A-395934
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US-11-266-748A-395934/c
; Sequence 395934, Application US/11266748A
; Publication No. US20060134663A1
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                                                                                                                                                                                       Query Match
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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Best Local Similarity
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 483996
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                                                                                                                                                                       Local
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                                                                         738
678 CTTCCTTATATATCAATTCTTT
                                   690 CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                           630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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l Similarity 69.5%;
57; Conservation
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                                                                         CTAAAGGAGGGCTGCCCCGTATAACTCCATTCTTGGTTCTCTCCTCCAAGTCCATAA
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Mulligan, Karl
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Pred. No. 0.6;
0; Mismatches
                                                                                                                                                                     Score 42; I
Pred. No. 1;
                                                                                                                                                   Mismatches
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RESULT 31 US-11-266-748A-466980

Sequence 466980, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:

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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 219
LENGTH: 1417
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LENGTH: 1000
                                                    Query Match
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ORGANISM: Homo Sapiens
-11-266-748A-466980
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SOFTWARE: PatentIn version 3
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                    NAME/KEY: CDS
LOCATION: (18)...(1172)
OTHER INFORMATION: JNK1 variant 2
                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                               TYPE: DNA
5.2%;
Local Similarity 69.5%;
hes 57; Conservative
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APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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APPLICATION NUMBER: EP 04105507.0
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APPLICATION NUMBER: EP 04105484.2
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Mulligan, Karl
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o. US20060134670A1
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           Score 42; DB 8; Length 1417; Pred. No. 1.1; 0; Mismatches 25; Indels
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Pred. No.
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APPLICANT: Uninston, Patrick
APPLICANT: Whiligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.0
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; ORGANISM: Homo sapiens
; PRATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1172)
; OTHER INFORMATION: JNK1 variant 3
US-11-283-329-221
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; Sequence 349577, Application US/11266748A
; Publication No. US20060134663A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 1417
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APPLICANT: Piu, Fabrice
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CURRENT FILING DATE: 2005-11-18
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PRIOR FILING DATE: 2004-11-19
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
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Local Similarity 69.5%;
ses 57; Conservative 0
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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US-11-266-748A-349577
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 349577
SEQ ID NO 349577
                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                   LENGTH: 1943
TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-382413
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Best Local :
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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APPLICANT: Johnston, P
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876 CTTCCTTATATATCAATTCTTT 855
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Similarity 69.5%;
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                                      CTTCCTTGTAGATAAGTTCTGT 711
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Pred. No. 1.2;
0; Mismatches 2
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ARPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: B0 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
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US-11-266-748A-432956
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Matches
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR FILING DATE: 2004-11-03 PRIOR FILING DATE: 2004-11-03 PRIOR PRIOR DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105483.4 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEO ID NOS: 483996

SOFTWARE: PatentIn version 3.3

SEO ID NO 24382
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; ORGANISM: Homo Sapiens
US-11-266-748A-24382
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SEQ ID NO 1069
LENGTH: 807
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Best Local Similarity
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ORGANISM: Glycine max
-11-216-545-1069
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Best Local
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APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
TITLE OF INVENTION: Soybeans.
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
PRIOR FILING DATE: 2004-08-31
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                                    476 AAGAAATAAAACTAAAATCATTATAAGGACACAA 509
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                                                                                                            356 CTTTAGCCCATGTTAACATTTTCTTCAGGATTCATTAACTATTAAAATTATTATGAAAAA 415
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Pred. No. 1.5;
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Pred. No. 1.5;
D; Mismatches 108;
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; NAME/KEY: misc feature
; LOCATION: (564)..(564)
; OTHER INFORMATION: n is
US-11-266-748A-207992
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APPLICANT: Mulligan, Karl
ITTLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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US-11-266-748A-207992/c
US-11-266-748A-207992/c
; Sequence 207992, Application US/11266748A
; Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILLING DATE: 2004-11-03
PRIOR PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
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APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                            Matches 107;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2005-07-1
NUMBER OF SEQ ID NOS: 483996
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NAME/KEY: misc_feature
LOCATION: (462)..(462)
OTHER INFORMATION: n is
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ORGANISM: Homo Sapiens
                                                                                                                                   491
                                                                                                                                                                                                                                                                                                               371 ACATTTTCTTCAGGATTCATTACTATTAAAATTATTTATGAAAAAGTTTTTGTCCTGGAT 430
165
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                                                                                                                                                                                                                                                                     345 ATATTTACAACAGTCATCTTCAAAATTGAAAAAGTGATTCAAGAACTTTGGATCTATTT
                                                                                                                              AATCATTATAAGGACACAACCATGTGATATTTGTCCATCTGCTCTTTAAGCAATGTTATG
                                                                                                                                                                              CATTGTTATAATTAGAGCCTTAAGTTGTGGGACTTTTATTCTTATTATATACTATATAAA
  TTTATTGGTACATCACAATAAGATAGTGTTAAATATT 129
                                          TTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATT 587
                                                                                       ATTTGTTCATGCTTTAATTTTTTCTGATTTGTTTCAATGTGGGTTTTTTGTTTTGTTTTG
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ilarity 49.3%;
Conservative
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Pred. No. 1.5;
0; Mismatches 110;
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RESULT 40 US-10-539-228-134/c

Sequence 134,

CAL INFORMATION:

Application US/10539228 b. US20060154250A1

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US-11-222-810-10
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; ORGANISM: Homo sapiens
US-11-222-810-10
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                                                                                                                                   Matches 80;
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Publication No.
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Best Local :
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APPLICANT: MUNNICH, Arnold
APPLICANT: MUNNICH, Arnold
TITLE OPI INVENTION: Spinal Muscular Atrophy Diagnostic Methods
FILE REFERENCE: 2121-0140P
CURRENT FILING DATE: 1055-09-12
CURRENT FILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: US/09/109,082
PRIOR APPLICATION NUMBER: US/09/109,082
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 08/545,196
PRIOR FILING DATE: 1995-10-19
NUMBER OF SEG ID NOS: 65
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SEQ ID NO 134
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APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: CHIR0052-101 (PP023370.0003)
CURRENT APPLICATION NUMBER: US/10/539,228
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 866
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OTHER INFORMATION: n = A,T,C or
.10-539-228-134
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NAME/KEY: misc_feature
/// /11932
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                                                                                                                                Local Similarity 54.8
188 80; Conservative
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                                                       424 CCTGGATCATTACCATCAGAATAATCAGAATGAATGCCACACTGAATATCAAAAGAAATA 483
                                                                                            139326
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                                                                                                                                                   54.8%;
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                                                                                                                                Score 40.4; DB Pred. No. 2.8; 0; Mismatches
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Pred. No. 9;
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2
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US-11-222-810-12
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APPLICANT: Johnston, P
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APPLICANT: MUNNICH, Arnold
TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
FILE REFERENCE: 2121-0140P
CURRENT APPLICATION NUMBER: US/11/222,810
CURRENT FILING DATE: 2005-09-12
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/109,082
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 08/545,196
PRIOR FILING DATE: 1995-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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TYPE: DNA
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APPLICATION NUMBER: US 60/662,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1543
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Mulligan, Karl
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Pred. No. 2.
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION UNMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105486.9
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; ORGANISM: Homo Sapiens
US-11-266-748A-41216
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SEQ ID NO 41216
LENGTH: 557
                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 95203
                                                                                                                                                                           Matches 63;
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
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FILING DATE: 2005-03-14
APPLICATION NUMBER: US 60/700,293
FILING DATE: 2005-07-18
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
168
                                       756 CACAGGGAAATTCATTACTTAATGCCAAATAATTACGTTTTG 797
                                                                                   228
                                                                                                                      696 TGTAGATAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATC 755
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CACAATTAAGTACAATTATTTATGGAGAAAAATTTTACTATG
                                                                                   CACAATTAAGTACAATTATTTATGGAGAAAATTTTTACTATG 132
                                                                                                                                                                           Conservative
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Pred. No. 3.
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Pred. No. 3.2;
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION UNMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105486.9
PRIOR APPLICATION NUMBER: EP 04105486.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105486.9
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 0410549.0
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR APPLICATION NUMBER: EP 04105403.6
PRIOR APPLICATION NUMBER: EP 04105405.0
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105405.0
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; Sequence 117427, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-148014
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Best Local S
Matches 63
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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Mulligan, Karl
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; ORGANISM: Homo Sapiens
US-11-266-748A-117427
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SEQ ID NO 159591
                                                                                              Best Local
                                                                                                              Query Match
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                                                                                                                                                  ORGANISM: Homo Sapiens
-11-266-748A-159591
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2005-07-1
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                     TYPE: DNA
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nes 63; Conservative
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APPLICATION NUMBER: EP 04105484.2
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/662,276 FILING DATE: 2005-03-14
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                                                                                              Similarity
TGTAGATAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATC 755
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                                                                                          Score 39.6;
Pred. No. 3.
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Pred. No. 3
                                                                         Mismatches
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US-11-266-748A-289193/c; Sequence 289193, Application US/11266748A; Publication No. US20060134663A1; GENERAL INFORMATION:
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US-11-266-748A-222651
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; Sequence 222651, Application US/11266748A

; Publication No. US20060134663A1
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Best Local (
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                                                         APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                        PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2005-07-18
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
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Local Similarity 61.8%;
es 63; Conservation
APPLICATION NUMBER: EP 04105482.6
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APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105507.0

APPLICATION NUMBER: EP 04105485.9

2004-11-03

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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-340622
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; ORGANISM: Homo Sapiens
US-11-266-748A-289193
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Best Local Similarity 61.8
Matches 63; Conservative
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SEQ ID NO 289193
                                           Query Match
                                                                                                                                                                           SEQ ID NO 340622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03 PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105482.6 PRIOR FILING DATE: 2004-11-03 PRIOR FILING DATE: 2004-11-03 PRIOR PILING DATE: 2004-11-03 PRIOR PILING DATE: 2004-11-03 PRIOR PILING DATE: 2004-11-03
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
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SOFTWARE: PatentIn version 3.3
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Local Similarity 61.0 nes .63; Conservative
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
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APPLICATION NUMBER: EP 04105507.0
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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APPLICATION NUMBER: US 60/662,276
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